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Relation of isozyme genotypes to quantitative characters in soybean

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Relation of isozyme genotypes to quantitative characters in soybean

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INTRODUCTION

The genetic improvement of crops depends on the availability of useful variability and techniques that allow effective selection among segregates in a population. Exploitation of polymorphisms that exist at the protein and DNA levels in a species may provide a means to increase the efficiency of plant improvement through development of marker-based selection schemes. The possibility has prompted considerable research using proteins, such as isozymes, as markers of the genome. Isozyme loci are used in cultivar identification, genetic linkage studies, as genetic markers in plant breeding and tissue culture, and in taxonomic and evolutionary studies. In addition, several studies have investigated the association between discrete isozyme loci and genes controlling the expression of quantitative characters.

Marker-based selection schemes may enhance the effectiveness of breeding procedures. A useful marker is one that allows unambiguous identification of all genotypes, has no pleiotropic effect, and no epistatic interaction with other markers, thus allowing the simultaneous identification of a large number of segregating marker loci. A desirable situation is to have many marker genes distributed throughout the genome in a manner that allows identification of any region of the genome by association with specific markers. An increase in the number of markers improves genome coverage and enhances the probability that a marker gene is linked with genes that affect other traits, particularly quantitative traits.

Proteins such as isozymes may be valuable for use as markers.

Isozymes are defined as "multiple molecular forms of an enzyme occurring within a single species as a result of the presence of more than one structural gene" (IUPAC-IUB, 1977). The multiple genes may be due to the presence of multiple gene loci or multiple alleles. The term allozyme is used to denote isozymes that are the product of allelic genes. Structural differences may arise as a result of variations in the primary structure of the protein (the amino acid sequence), differences in secondary or tertiary structure, or, in polymeric enzymes, from the association of different subunits to produce an array of quaternary structures. The association of nonidentical subunits to form catalytically active molecules frequently accounts for the existence of multiple forms of enzymes. Electrophoresis is the most common method used for the identification of variant enzyme forms (Moss, 1982).

Isozymes are simply inherited and usually exhibit codominance, allowing identification of both homozygous and heterozygous loci. Unlike genes controlling morphological traits, genes that are responsible for the production of isozymes generally do not exhibit pleiotropic or epistatic effects, so several loci may be evaluated simultaneously. For alleles that are codominant or partially dominant, the genotype of an individual with respect to isozyme loci can be directly inferred from the phenotype observed on the electrophoretic gel; the heritability is 100%.

Many characters of economic importance in crop plants exhibit a quantitative pattern of inheritance. The number of segregating loci influencing a quantitative trait is generally too large to identify

discrete phenotypic classes. Because of the number of segregating loci, and the effect that environmental factors have on obscuring any differences among phenotypic classes, quantitative traits typically show continuous variation for the character being evaluated. Thus, phenotypes must be evaluated in replicated tests over multiple environments to identify superior genotypes. A relationship between isozyme loci and quantitative traits could increase the efficiency and effectiveness of genetic improvement.

To be of practical use in marker-based selection schemes, associations between isozyme loci and quantitative traits must be applicable to the desired breeding systems. Much of the work on relation of isozyme genotypes to quantitative traits in breeding populations of allogamous species has been conducted in maize. The populations studied included random mating populations, populations undergoing recurrent selection based on evaluation of half-sib, full-sib, or selfed progenies, and F2 populations derived from the cross of two inbred lines. For autogamous species, studies investigating the use of isozymes to locate genes affecting quantitative characters have been conducted to the greatest extent in tomato, where interspecific crosses were used to generate sufficient polymorphism for isozyme alleles and morphological characters.

Soybean is an autogamous species belonging to the genus Glycine Willd., which is composed of two subgenera, Glycine and Soja (Moench) F. J. Hermann (Hymowitz and Newell, 1981; Ladizinsky et al., 1979; Newell and Hymowitz, 1982). The subgenus Soja contains two annual species: G. max, the cultivated soybean, and G. soja, the wild species. Glycine soja is a potential source of new germplasm in soybean

breeding programs.

The wild soybean is a viny plant with no main stem, small seeds, colored seedcoats and shattering pods; it is very agronomically undesirable. The cultivated soybean, G. max, has an upright main stem and has been selected for desirable agronomic traits.

In a study that examined different backcross populations from two G. max x G. soja crosses for occurrence of agronomically desirable segregates, Ertl and Fehr (1985) found that the BC2, the second backcross generation, was the first generation that had segregates that were similar to the recurrent parent for yield, maturity, lodging, and plant height. The frequency of those lines was 4% in the BC2 and 25% in the BC3. Carpenter and Fehr (1986) evaluated the plant type of random F3 lines from backcross populations of the same two interspecific crosses. They found no segregates with a plant type similar to the G. max parent until the BC2 generation, where 4% of the lines were similar to the G. max parent in one cross.

The cultivated and wild species differ for morphological characters and possess different alleles at several isozyme loci. Marker loci may be useful in an introgression program to enhance the recovery of the recurrent parent phenotype and decrease the number of lines that is evaluated in the field.

There are no reports of the association between marker loci and quantitative traits in soybean. The objectives of my study were (1) to examine the relationship between agronomic performance and the number of isozyme marker loci that are homozygous for G. soja isozyme

alleles, and (2) to determine if particular marker loci or genes linked to them affected specific quantitative traits.

LITERATURE REVIEW

Associations between single, easily identified genes and genes affecting agronomic traits that are inherited quantitatively could increase the efficiency and effectiveness of selection. The value of associations between genes that could be easily identified and genes that affect quantitative characters was recognized early in this century. Sax (1923) reported an association between seed size and pigmentation in Phaseolus vulgaris L. He stated that if "certain size factors can be found linked with factors for qualitative characters it should be possible to study independently the size factor or factors within each linkage group. This is now possible in a limited way with the size differences in beans." Everson and Schaller (1955) investigated an association between semi-smooth awns and high yield in barley. They reported that the effect was not due to pleiotropic action of the semi-smooth gene (r) itself, but to linkage of the r gene with genes affecting yield.

The markers used in early studies were genes, usually mutant alleles, that produced a recognizable effect on the phenotype of the individual. Extensive work on the association between marker genes and genes influencing quantitative characters was limited to organisms like Drosophila that had an abundance of morphological markers. Thoday (1961) discussed the use of markers to locate polygenes. Spickett and Thoday (1966) used the principles described by Thoday (1961) to locate genes affecting sternopleural cheta number in Drosophila melanogaster. They located one gene on chromosome II, two on chromosome III, and two

on the X chromosome. The five genes accounted for 87.5% of the difference between the parents for the trait. They stated that the polygenes that could be located using these techniques were probably a "non-random sample comprising the most extremely effective genes or linked complexes of a continuous spectrum which ranges down to genes of vanishingly small effect" (Spickett and Thoday, 1966).

In plant species, Wehrhahn and Allard (1965) used inbred backcross lines to detect genes affecting heading date in wheat (Triticum aestivum L.). They identified four loci, or effective factors, that had large effects on heading date. One of the loci accounted for 80% of the total additive variance expressed, and the other three loci together accounted for about 14% of the additive variance. Law (1966) identified a factor, E, that had a large effect on heading date in wheat, and located it on chromosome 7B linked with a gene for purple culm (Pc). Law (1967) used the same experimental material, an intervarietal chromosome substitution line, to determine the positions of genes affecting five quantitative traits. He was able to locate chromosomal segments affecting height, grain number, and tiller number based on their associations with four genetic markers on chromosome 7B.

The numbers of markers used in any of these studies was small relative to the size of the genome. Even for Drosophila, Thoday (1961) stated that the main practical limitation of the use of markers to locate polygenes was the availability of suitable markers. Faced with a similar paucity of good markers, Hubby and Lewontin (1966) described the use of electrophoretic mobility variants to study heterozygosity in natural populations of Drosophila pseudoobscura. The authors listed

four criteria that had to be met for a technique to be useful in studying the amount of heterozygosity per locus in a population. First, "Phenotypic differences caused by allelic substitutions at single loci must be detectable in single individuals." Second, "Allelic substitutions at one locus must be distinguishable from substitutions at other loci." Third, "A substantial portion of (ideally, all) allelic substitutions must be distinguishable from each other." Fourth, "Loci studied must be an unbiased sample of the genome with respect to physiological effects and degree of variation" (Hubby and Lewontin, 1966).

The properties of many isozyme loci satisfy these criteria. Unlike many morphological mutants, alleles at isozyme loci are codominant, so all genotypes at a locus can be identified. The pleiotropic and epistatic effects of many morphological markers make their use difficult and undesirable in many studies. Isozyme loci, however, generally do not exhibit pleiotropic effects or epistatic interactions, so a large number of loci can be studied simultaneously. Furthermore, with many enzyme loci of different catalytic activity, good distribution of the markers in the genome is possible (Tanksley, 1983).

Isozyme allele frequencies have been studied in natural plant populations. Marshall and Allard (1970) reported a significant correlation between polymorphic index values calculated for morphological markers and enzyme variants in two natural populations of oat (Avena spp.). Clegg and Allard (1972) found that allelic frequencies at five enzyme loci and two loci responsible for morphological variants were closely associated with the environment to which the population

was adapted. Hamrick and Allard (1975) reported correlations between quantitative characters and enzyme genotypes in natural populations of Avena barbata in California. In natural maize populations, Doebley et al. (1985) observed strong correlations between some isozyme alleles and altitude.

Associations between isozyme allele frequencies and morphological or quantitative traits have been studied in breeding populations. Brown (1971) examined allele frequencies at six loci in eight selected strains of maize from the long-term selection experiment at Illinois. He concluded that differentiation among the strains by allele frequencies at those six loci was not different from random genetic drift, but the deviations suggested that isozyme variants were not entirely neutral to selection. Brown and Allard (1971) reached a similar conclusion using nine isozyme loci as markers to monitor the genetic effects of two cycles of reciprocal recurrent selection in a population of maize. The changes in allele frequency at the marker loci could be ascribed to random genetic drift associated with the restriction of the population size at the time of selection. In an investigation of the relationships between nine enzyme loci and individual plant traits in two mass-selected maize populations, Pollak and Gardner (1986) found no significant relationships between the number of heterozygous enzyme loci and morphological traits. They pointed out that random mating would eliminate correlations between heterozygosity and single plant traits unless strong selection pressure, tight linkages, or nonrandom mating were significant factors. Kahler (1983) monitored the allele frequency at nine enzyme loci over eight cycles of selection

for grain yield in the maize population Krug BSK. Both half-sib and S_1 progeny evaluation were conducted. He concluded that stabilizing selection, random genetic drift, or both factors combined with undetected directional selection could account for the observed changes in allele frequency at the nine loci studied.

Stuber and his colleagues observed that alleles at enzyme loci were responsive to directional selection and were associated with changes in grain yield (Stuber and Moll, 1972; Stuber et al., 1980). They conducted an experiment to test the hypothesis that manipulation of frequencies of isozyme alleles would produce responses in correlated quantitative traits. In an experiment where selection was based solely on allelic frequencies at seven enzyme loci, Stuber et al. (1982) obtained an improvement in grain yield equivalent to one and one-half to two cycles of full-sib family selection for yield alone. Frei et al. (1986b) were successful at inducing yield changes by divergent selection based on seven allozyme loci in subpopulations of a composite formed from 30 elite corn lines. They noted that allozyme selection increased specific combining ability with B73 because the positive allozyme selections showed an upward trend when evaluated as B73 topcrosses, but a downward trend when evaluated as populations per se. They concluded that allozyme associations with yield existed, but further studies were necessary using other populations and testers.

Other studies in breeding populations of maize have focused on inbred lines, F_1 hybrids, and their F_2 populations. Kahler and Wehrhahn (1986) evaluated associations between eight enzyme loci and eleven quantitative traits in the cross between inbred lines Wf9 and Pa405.

They reported that all enzyme loci were strongly associated with at least one quantitative trait and all quantitative traits had significant associations with genotypes at particular enzyme loci in the F_2 population. They suggested the possible use of enzyme marker loci to identify inbred lines that would show good heterotic response in hybrid combinations. Price et al. (1986) concluded that allelic differences at enzyme loci between inbred lines of maize may not be useful as predictors of heterotic performance of single-cross hybrids. Frei et al. (1986a) found a relationship between hybrid vigor and dissimilarities of genotypes at allozyme loci, but the predictive power was questionable and depended on the pedigree background of the lines. Edwards et al. (1987) and Stuber et al. (1987) reported significant associations between isozyme marker loci and loci affecting quantitative traits in two F_2 populations of maize. The populations were segregating for seventeen or twenty marker loci, and Edwards et al. (1987) detected and mapped quantitative trait loci (QTL) for each of the 82 traits evaluated.

In autogamous crop species, much of the research on relation of isozyme genotypes to quantitative traits and location of QTL has been conducted in tomato. Tanksley and Rick (1980) discussed applications of isozyme analysis in plant breeding and genetics and its use for detecting introgression of genes from wild germplasm. Tanksley et al. (1981) found significant correlations between heterozygosity value and four metric characters in an interspecific backcross of tomato. The heterozygosity value was a measure of the number of loci with alleles from the wild species, Solanum pennellii. Tanksley et al. (1982)

detected and mapped at least 21 QTL in the interspecific backcross Lycopersicon esculentum X Solanum pennellii with respect to the 12 enzyme marker loci that were segregating in the cross. Vallejos and Tanksley (1983) used 11 segregating isozyme loci and identified at least three QTL that affected cold tolerance in the interspecific cross L. esculentum X L. hirsutum. Two of the detected QTL had positive effects and one had a negative effect on cold tolerance.

Relationships between isozyme loci and important traits have been used in plant improvement. In tomato, the Aps-1 allele can be used to select for nematode resistant plants because of linkage of the isozyme locus with the gene controlling nematode resistance (Rick and Fobes, 1974). Weeden et al. (1984) reported linkage of the isozyme locus, Pgm-p, with the locus controlling resistance to bean yellow mosaic virus (BYMV), Mo. The distance between the two loci is two recombination units, suggesting that the enzyme locus can be used as a genetic marker for resistance to BYMV.

There are no reports on associations between isozyme marker loci and quantitative characters in soybean. Like tomato, the isozyme polymorphisms that exist within the cultivated species are rare (Kiang and Gorman, 1983). To obtain segregation for many isozyme loci and quantitative characters, interspecific crosses can be used. Significant associations between isozyme genotypes and quantitative characters in the interspecific crosses could be useful in an introgression program, as suggested by Tanksley et al. (1982).

The traits evaluated in this study were maturity, height, lodging, plant type, and vining. Studies of the segregation of progenies from

crosses between G. max and G. soja indicated that these traits were influenced by many factors and the inheritance was complex. Tang and Li (1963) and Tang and Tai (1962) reported that approximately seven effective factors were responsible for the expression of maturity in the interspecific crosses, and that there was dominance for date of maturity. Weber (1950) reported no dominance for factors conditioning maturity in both single-cross and backcross populations. Transgressive segregation in both directions was observed (Weber, 1950; Williams, 1948).

Plant height measured on F_1 hybrids of G. max and G. soja was closest to the G. soja parent, but shifted toward the G. max parent with successive selfing generations (Tang and Tai, 1962; Ting, 1946). Ting (1946) considered height a quantitative trait controlled by a large number of genes. Tang and Tai (1962) estimated the number of effective factors to be 12.

Lodging, plant type, and vining are related to the growth habit of the plant. In G. max, lodging is considered a quantitative trait, and variation in degree of lodging is due mainly to additive effects (Brim, 1973; Johnson and Bernard, 1963). Carpenter and Fehr (1986) observed transgressive segregates with lodging scores 0.5 units better than the G. max parent in the BC_2 to BC_5 generations in one of the two interspecific crosses they studied. Tang and Chen (1959) reported that lodging, branching habit, and type of growth resembled the wild parent. Ting (1946) considered the inheritance of prostrate growth habit to be quantitative. The procumbent nature of the wild parent was observed

in the F_1, F_2, F_3, and BC_1 generations, indicating dominance for this trait in G. soja (Karasawa, 1936; Weber, 1950; Williams, 1948). Ting (1946) recovered erect plants in F_2 populations of crosses between G. soja and G. max, but the erect habit of the G. max parent was not recovered in the F_2, F_3, or BC_1 generations by Williams (1948). Carpenter and Fehr (1986) reported that 10% of the F_2-derived lines in the BC_1 generation were similar to the G. max parent for lodging score, but no lines were recovered until the BC_2 generation that were similar to the recurrent parent for agronomic score and vining score.

MATERIALS AND METHODS

Twenty plant introductions (PI) of the wild soybean (Glycine soja Sieb. and Zucc.) and 20 elite lines or cultivars of Glycine max (L.) Merr. were used to form 20 populations originating from interspecific crosses. The G. soja parents were of Maturity Groups 0 to III and either originated from different geographical regions or were introduced in different years. The G. max parents were of Maturity Groups I to III and were chosen for their superior yield potential and for differences in their ancestry.

Each of the 20 G. soja PI was crossed to one of the 20 G. max cultivars at Ames, Iowa during 1983. Twelve F_1 seeds per cross were obtained. Two backcrosses were made to the G. max parent to obtain progenies with a good range of phenotypes from G. max to G. soja for the quantitative traits evaluated (Carpenter and Fehr, 1986; Ertl and Fehr, 1985). The 20 single crosses were backcrossed during the winter at the Iowa State University-University of Puerto Rico Soybean Breeding Nursery at Isabela, Puerto Rico using their respective G. max parents as male. At least 32 BC_1F_1 plants from each population were grown at the Agronomy Research Center near Ames, Iowa during 1984, and 25 BC_2F_1 seeds were obtained for each cross, using as many BC_1F_1 plants as possible. BC_2F_1 plants were grown in Puerto Rico during the winter to obtain BC_2F_2 seeds.

To determine the isozyme genotype of the BC_2F_1 plants, three F_2 seeds from each F_1 plant were analyzed by starch gel electrophoresis (Cardy and Beversdorf, 1984). The objective was to identify plants

that possessed at least one allele from G. soja at a given locus. Because alleles in these enzymes exhibited codominance, the heterozygote could be identified on the electrophoretic gel. To identify an F_1 plant that contained a G. soja allele at a locus, F_2 seeds were analyzed. The probability of identifying an F_2 seed that has at least one G. soja allele is 0.75, because both the heterozygote and the homozygous G. soja class can be identified. To be 99% certain of recovering at least one F_2 seed that has a G. soja allele, three seeds have to be analyzed (Sedcole, 1977).

The enzymes that were assayed were aconitase [aconitate hydratase, enzyme commission (EC) 4.2.1.3, Aco2, Aco4 loci] acid phosphates (EC 3.1.3.2, Ap locus), diaphorase (EC 1.6.4.3, Dia1 locus), endopeptidase (Enp locus), defined as an enzyme capable of hydrolyzing BANA (α-N-benzoyl-DL-arginine-β-naphthylamide), isocitrate dehydrogenase (EC 1.1.1.42, Idh1, Idh2 loci), phosphoglucomutase (EC 2.7.5.1, Pgm1 and Pgm2 loci), phosphoglucose isomerase (EC 5.3.1.9, Pgi locus) and malate dehydrogenase (MDH). Malate dehydrogenase mobility variants were observed, but no formal designations have been made for loci or alleles in soybean. As a conservative estimate, a single locus was assumed to condition the electrophoretic variants that were observed. The eight enzymes were chosen because their resolution on starch gel electrophoresis was consistent and only two different gel systems were needed to assay all the enzymes at the same time (Cardy and Beversdorf, 1984). Additional enzymes were not consistently well-resolved and required separate gel systems for their analysis, so they were not well-suited for use in a study that required evaluation of thousands of genotypes.

After analysis of the 20 G. soja and 20 G. max parents using eight enzyme systems, eight populations were chosen for further study because they possessed five or more segregating isozyme loci. One hundred BC_2F_2 seeds from every BC_2F_1 plant of the eight populations were grown at Ames during 1985. Isozyme analysis of remnant seed from BC_2F_1 plants was conducted during the summer of 1985 to determine which BC_2F_1 families were segregating for the isozyme alleles for which the parents differed. After isozyme analysis of a total of 353 BC_2F_1 families from the eight crosses, two crosses with the greatest number of heterozygous isozyme loci in the BC_2F_1 generation were chosen for use in this study.

For Cross 1, the experimental line A80-244036 and PI 326581 possessed different alleles at six of the isozyme loci that were tested: Aco2, Idh2, Ap, Pgm1, Pgm2, and Pgi. BC_2F_1 families were identified that had G. soja alleles at up to five of the six loci. For Cross 2, the experimental line A81-157007 and PI 342618A differed for alleles at eight isozyme loci tested: Aco2, Aco4, Idh1, Dia1, Ap, Pgm1, Pgm2, and MDH. BC_2F_1 families were identified that had G. soja alleles at up to six of the eight loci. The line A80-244036 is an elite line of Maturity Group II, and A81-157007 is an elite line of Maturity Group I. The two PI belong to Maturity Group II and were introduced from the U.S.S.R.

From each population, 10 BC_2F_1-derived lines that had the greatest number of heterozygous isozyme loci were inbred by single seed descent to the F_4 generation to increase the frequency of homozygous isozyme loci. The generation advance was conducted at the Iowa State University-

University of Puerto Rico Soybean Breeding Nursery at Isabela, Puerto Rico during November 1985 to May 1986. From each BC_2F_1-derived line, five BC_2F_4 plants with different numbers of marker loci homozygous for G. soja alleles were desired.

The expected frequencies of loci homozygous for G. soja alleles in the BC_2F_4 generation were calculated to determine the number of seeds and plants that should be grown each generation assuming 70% germination in Puerto Rico (Tables 1 and 2). For a single locus with two alleles, if the BC_2F_1 plant is heterozygous, the frequency of the two homozygous classes in the F_4 generation will be 7/16. The multilocus genotype frequencies can be determined by expansion of the binomial $(p + q)^n$, where $p = q = 7/16$ is the probability of a locus that is homozygous for G. max alleles (p) or G. soja alleles (q) in the BC_2F_1 generation, and n is the number of heterozygous loci in the BC_2F_1 plant. It is evident that for any number of heterozygous isozyme loci in the BC_2F_1 generation, the extreme classes of homozygous isozyme loci in the BC_2F_4 generation were the most difficult to obtain. Calculations of the numbers of seeds and plants necessary for each generation were based on the frequencies of these extreme classes. For example, a BC_2F_1 plant from Cross 2 had six heterozygous isozyme loci. The probability of recovering a BC_2F_4 plant that had zero isozyme alleles from G. soja was less than 1/64 (Table 1). This was equal to the probability of obtaining a BC_2F_4 plant from this BC_2F_1-derived line that was homozygous for G. soja alleles at all 6 isozyme loci. To be 99% certain ($p = 0.99$) of obtaining 5 BC_2F_4 plants ($r = 5$) that were homozygous at all 6 loci ($q = 1/64$), 739 BC_2F_4 plants were required (Sedcole, 1977). Similar

Table 1. Frequency of plants homozygous for *G. soja* alleles at different numbers of loci in the BC_2F_4 generation

Number of heterozygous BC_2F_1 loci	No. of homozygous loci in BC_2F_4[a]						
	0	1	2	3	4	5	6
0	1.0000						
1	0.4375	0.4375					
2	0.1914	0.3828	0.1914				
3	0.0837	0.2511	0.2511	0.0837			
4	0.0366	0.1464	0.2196	0.1464	0.0366		
5	0.0160	0.0800	0.1600	0.1600	0.0800	0.0160	
6	0.0070	0.0420	0.1050	0.1400	0.1050	0.0420	0.0070

[a]Number of isozyme marker loci that were homozygous for alleles from *G. soja*.

calculations were made for each of the locus classes (Table 2).

Field evaluation and analysis of isozyme genotypes of BC_2F_4-derived lines were conducted during the same season, so the marker-locus genotypes of the lines were not known until after harvest. Three thousand nine hundred and seventy-four BC_2F_4-derived lines were grown in two replications at two locations in Iowa during 1986. For each cross, BC_2F_4-derived lines in a BC_2F_1 family were divided equally among sets of 110 entries so that lines with different numbers of loci homozygous for G. soja alleles had equal opportunity to occur in each set. There was one entry of each parent in every set. Fifteen seeds were planted in single-row plots that were 76 cm long and spaced 69 cm apart.

Remnant BC_2F_5 seeds were used for isozyme analysis. Four seeds from every BC_2F_4 plant were used to determine their isozyme genotypes. Because of the inheritance of the enzymes used, all genotypic classes at a locus could be identified for an individual. To decrease the number of isozyme assays, a sample from one cotyledon from each of the four seeds was placed in a single tube and treated as one sample for electrophoresis. This procedure allowed identification of heterozygous BC_2F_4 plants, even with only one heterozygous seed and three homozygous seeds for a given isozyme locus.

Data for the following agronomic traits were recorded for each plot:

Date of maturity (MAT) — recorded as the number of days after 31 August when 95% of the pods on the main stems of the plants in a plot had reached their mature color. For plants without a distinct main stem, the date of maturity was considered to be when 95% of the pods

Table 2. Number of plants required for each generation of inbreeding by single seed descent to be 99% certain of recovering five BC_2F_4 plants in each locus class

Cross	BC_2F_1 plant	No. of heterozygous BC_2F_1 loci	BC_2F_2	BC_2F_3	BC_2F_4
1	1	5	536	376	268
	2, 3	4	364	255	182
	4, 5, 6	3	178	125	89
	7-10	2	86	61	43
2	1, 2	6	1478	1035	739
	3	5	536	376	268
	4-10	4	364	255	182

on the plant had reached their mature color.

Plant height (HT) — measured as the length of the main stem, or longest branch if there was no main stem, from the soil surface to the stem tip. The value for HT was calculated from the average of three plants in a plot and was measured in centimeters.

Lodging score (LDG) — a visual rating to the nearest 0.1 of the average angle of the plants in a plot to the ground, based on a 1 to 5 scale with 1 designating all plants erect and 5 all plants prostrate.

Plant type (PLT) — the agronomic desirability of a line based on a 1 to 5 scale with 1 representing a *G. max* type and 5 representing a *G. soja* type.

Vining score (VNG) — the growth habit of a plant measured on a 1 to 5 scale with 1 representing types with an upright main stem and no vining side branches, and 5 representing a plant with no main stem that is procumbent.

After collection of field and isozyme data for every BC_2F_4-derived line, lines for each locus class were selected for data analysis. The 0-locus class represented random lines that had retained no *G. soja* alleles at any of the marker loci. The 1-locus class consisted of lines that were homozygous for *G. soja* alleles at one of the marker loci, and homozygous for *G. max* alleles at all other marker loci. The 2-locus class contained lines that were homozygous for *G. soja* alleles at two of the isozyme marker loci and homozygous for *G. max* alleles at all other marker loci. The 3-, 4-, and 5-locus classes consisted of lines that were homozygous for *G. soja* alleles at that number of isozyme loci and for *G. max* alleles at the remaining loci.

Selection of lines for data analysis was based on their isozyme genotypes. For the 0-locus class, five lines from each of the ten BC_2F_1 families were used. For the 1-, 2-, 3-, 4-, and 5-locus classes, at least two but no more than five lines were chosen from as many families as possible for each enzyme genotype within the locus class. For example, six different enzyme genotypes were recovered in the 1-locus class for Cross 1 and eight different enzyme genotypes were recovered in the 1-locus class for Cross 2. As many multilocus combinations as possible were represented in the 2-, 3-, 4-, and 5-locus classes.

Means and standard errors for all traits at individual environments and averaged across environments were calculated using PROC MEANS in SAS (SAS User's Guide: Basics, Version 5 Edition, 1985). Means and standard errors for each trait were calculated for every enzyme genotype and locus class both within each family and over all families for a cross.

Analyses of variance were performed on all traits at individual environments and combined over environments. For all analyses, entries and locations were assumed to be random effects and loci and enzymes were considered fixed effects. Analyses of variance were performed using PROC ANOVA in SAS (SAS User's Guide: Statistics, Version 5 Edition, 1985).

Data for the parents of a cross, which were the common entries in each set, were analyzed to determine if set differences were important. An analysis of variance for the parental genotypes was performed according to the model:

$$Y_{ijkl} = u + L_i + R_{ij} + S_k + G_l + (SG)_{kl} + (LS)_{ik} + (LG)_{il} + (LSG)_{ikl} + e_{ijkl}$$

where: Y_{ijkl} = observed value of the lth genotype in the kth set in the jth replication of the ith location;

u = overall mean;

i = 1 to 2;

j = 1 to 2;

k = 1 to 11 for Cross 1; k = 1 to 30 for Cross 2;

l = 1 to 2;

L_i = effect of the ith location;

R_{ij} = effect of the jth replication in the ith location;

S_k = effect of the kth set;

G_l = effect of the lth genotype;

$(SG)_{kl}$ = effect of the interaction of the kth set with the lth genotype;

$(LS)_{ij}$ = effect of the interaction of the ith location with the jth set;

$(LG)_{il}$ = effect of the interaction of the ith location with the lth genotype;

$(LSG)_{ikl}$ = effect of the interaction of the ith location with the kth set and the lth genotype;

e_{ijkl} = effect of the error associated with the ijklth observation.

The F test for significance of the mean squares for sets was tested with the location x set mean squares (Table 3). Because no

Table 3. Analysis of variance for parental genotypes

Sources of variation	Degrees of freedom	Expectations of mean squares
Location (L)	(l-1)	
Replication/L (R/L)	l(r-1)	
Set (S)	(s-1)	$\sigma_e^2 + e\sigma^2_{(R/L)S} + re\sigma^2_{LS} + rle\sigma^2_s$
Genotype (G)	(g-1)	$\sigma_e^2 + s\sigma^2_{(R/L)G} + r\sigma^2_{LSG} + rs\sigma^2_{LG} + Rl\sigma_{SG} + rls[G^2/(g-1)]$
S X G	(s-1)g-1)	$\sigma_e^2 + r\sigma^2_{LSG} + rl\sigma^2_{SG}$
L X S	(l-1)(s-1)	$\sigma_e^2 + e\sigma^2_{(R/L)S} + re\sigma^2_{LS}$
L X G	(l-1)(g-1)	$\sigma_e^2 + s\sigma^2_{(R/L)G} + r\sigma^2_{LSG} + rs\sigma^2_{LG}$
L X S X G	(l-1)(s-1)(g-1)	$\sigma_e^2 + r\sigma^2_{LSG}$
Error	l(r-1)(sg-1)	σ_e^2

significant differences were observed, data for the lines were analyzed according to a randomized complete block design with no correction for sets from which the lines were selected.

Data of the BC_2F_4-derived lines were analyzed at individual locations according to the model:

$$Y_{ijkl} = u + R_i + L_j + E_{jk} + G_{ijk} + (RL)_{ij} + (RE)_{ijk} + (RG)_{ijkl}$$

where: Y_{ijkl} = observed value of the lth genotype in the kth enzyme class in the jth locus class in the ith replication;

u = overall mean;

i = 1 to 2;

j = 0 to 5;

k = 1 to 14 for Cross 1; k = 1 to 24 for Cross 2;

l = 1 to 49 for Cross 1; l = 1 to 36 for Cross 2;

R_i = effect of the ith replication;

L_j = effect of the jth locus class;

E_{jk} = effect of the kth enzyme class in the jth locus class;

G_{jkl} = effect of the lth genotype in the kth enzyme class in the jth locus class;

$(RL)_{ij}$ = effect of the interaction of the jth locus class with the ith replication;

$(RE)_{ijk}$ = effect of the interaction of the kth enzyme class in the jth locus class with the ith replication;

$(RG)_{ijkl}$ = effect of the interaction of the lth genotype in the kth enzyme class in the jth locus class with the ith replication.

In the analysis of variance, the mean squares due to enzyme class, genotype within enzyme class, and their interactions with replications were each subdivided into six components corresponding to the six locus classes, 0, 1, 2, 3, 4, and 5.

The significance of the locus-class effect was tested with the replication x locus-class interaction mean squares. The significance of the enzyme-class effect was tested using an approximate F test (Satterthwaite, 1946), where

$F'_{p,q} = (M1 + M5)/(M2 + M4)$ and

M1 = enzyme within loci mean square;

M2 = genotype within enzyme within loci mean square;

M4 = replication x enzyme within loci mean square;

M5 = replication x genotype within enzyme within loci mean square.

The appropriate degrees of freedom for the F' statistic were calculated according to Satterthwaite (1946) as follows:

$$p = (M1 + M5)^2/[(M1^2/f_1) + (M5^2/f_5)]$$

$$q = (M2 + M4)^2/[(M2^2/f_2) + (M4^2/f_4)]$$

where f_1, f_2, f_4, and f_5 are the degrees of freedom for the corresponding mean squares (Table 4). The significance of the genotype effect was tested against the replication x genotype within enzyme within loci mean squares.

Data for the BC_2F_4-derived lines were combined across locations according to the model:

Table 4. Analysis of variance for BC_2F_4-derived lines for individual locations

Sources of variation	Degrees of freedom
Replication (R)	(r-1)
Entry (V)	(v-1)
Loci (L)	(1-1)
Enzyme/Loci (E/L)	1(e-1)
E/L=0	(e_0-1)
E/L=1	(e_1-1)
E/L=2	(e_2-1)
E/L=3	(e_3-1)
E/L=4	(e_4-1)
E/L=5	(e_5-1)
Genotype/Enzyme/Loci (G/E/L)	1e(g-1)
G/E/L=0	$e_0(g_0-1)$
G/E/L=1	$e_1(g_1-1)$
G/E/L=2	$e_2(g_2-1)$
G/E/L=3	$e_3(g_3-1)$
G/E/L=4	$e_4(g_4-1)$
G/E/L=5	$e_5(g_5-1)$

Expectations of mean squares	Mean squares
$\sigma_e^2 + v\sigma_R^2$	
$\sigma_e^2 + r\sigma_V^2$	
$eg\sigma_{RL}^2 + L^2/(l-1)$	
$\sigma_{RG/E/L}^2 + g\sigma_{RE/L}^2 + r\sigma_{G/E/L}^2 + rg(E/L)^2/[l(e-1)]$	M1
$\sigma_{RG/E/L=0}^2 + g_0\sigma_{RE/L=0}^2 + r\sigma_{G/E/L=0}^2 + rg_0(E/L=0)^2/(e_0-1)$	
$\sigma_{RG/E/L=1}^2 + g_1\sigma_{RE/L=1}^2 + r\sigma_{G/E/L=1}^2 + rg_1(E/L=1)^2/(e_1-1)$	
$\sigma_{RG/E/L=2}^2 + g_2\sigma_{RE/L=2}^2 + r\sigma_{G/E/L=2}^2 + rg_2(E/L=2)^2/(e_2-1)$	
$\sigma_{RG/E/L=3}^2 + g_3\sigma_{RE/L=3}^2 + r\sigma_{G/E/L=3}^2 + rg_3(E/L=3)^2/(e_3-1)$	
$\sigma_{RG/E/L=4}^2 + g_4\sigma_{RE/L=4}^2 + r\sigma_{G/E/L=4}^2 + rg_4(E/L=4)^2/(e_4-1)$	
$\sigma_{RG/E/L=5}^2 + g_5\sigma_{RE/L=5}^2 + r\sigma_{G/E/L=5}^2 + rg_5(E/L=5)^2/(e_5-1)$	
$\sigma_{RG/E/L}^2 + r\sigma_{G/E/L}^2$	M2
$\sigma_{RG/E/L=0}^2 + r\sigma_{G/E/L=0}^2$	
$\sigma_{RG/E/L=1}^2 + r\sigma_{G/E/L=1}^2$	
$\sigma_{RG/E/L=2}^2 + r\sigma_{G/E/L=2}^2$	
$\sigma_{RG/E/L=3}^2 + r\sigma_{G/E/L=3}^2$	
$\sigma_{RG/E/L=4}^2 + r\sigma_{G/E/L=4}^2$	
$\sigma_{RG/E/L=5}^2 + r\sigma_{G/E/L=5}^2$	

Table 4. Continued

Sources of variation	Degrees of freedom
Error (R X V)	(r-1)(v-1)
R X L	(r-1)(1-1)
R X E/L	1(r-1)(e-1)
R X E/L=0	(r-1)(e_0-1)
R X E/L=1	(r-1)(e_1-1)
R X E/L=2	(r-1)(e_2-1)
R X E/L=3	(r-1)(e_3-1)
R X E/L=4	(r-1)(e_4-1)
R X E/L=5	(r-1)(e_5-1)
R X G/E/L	1e(r-1)(g-1)
R X G/E/L=0	e_0(r-1)(g_0-1)
R X G/E/L=1	e_1(r-1)(g_1-1)
R X G/E/L=2	e_2(r-1)(g_2-1)
R X G/E/L=3	e_3(r-1)(g_3-1)
R X G/E/L=4	e_4(r-1)(g_4-1)
R X G/E/L=5	e_5(r-1)(g_5-1)

Expectations of mean squares	Mean squares
σ^2_e	
$eg\sigma^2_{RL}$	M3
$\sigma^2_{RG/E/L} + g\sigma^2_{RE/L}$	M4
$\sigma^2_{RG/E/L=0} + g_0\sigma^2_{RE/L=0}$	
$\sigma^2_{RG/E/L=1} + g_1\sigma^2_{RE/L=1}$	
$\sigma^2_{RG/E/L=2} + g_2\sigma^2_{RE/L=2}$	
$\sigma^2_{RG/E/L=3} + g_3\sigma^2_{RE/L=3}$	
$\sigma^2_{RG/E/L=4} + g_4\sigma^2_{RE/L=4}$	
$\sigma^2_{RG/E/L=5} + g_5\sigma^2_{RE/L=5}$	
$\sigma^2_{RG/E/L}$	M5
$\sigma^2_{RG/E/L=0}$	
$\sigma^2_{RG/E/L=1}$	
$\sigma^2_{RG/E/L=2}$	
$\sigma^2_{RG/E/L=3}$	
$\sigma^2_{RG/E/L=4}$	
$\sigma^2_{RG/E/L=5}$	

$$Y_{ijklm} = u + A_i + R_{ij} + L_k + E_{kl} + G_{klm} + (AL)_{ik} + (AE)_{ikl} + (AG)_{iklm} + (RL)_{ijk} + (RE)_{ijkl} + (RG)_{ijklm}$$

where: Y_{ijklm} = observed value of the mth genotype in the lth enzyme class in the kth locus class in the jth replication in the ith location;

u = overall mean;

i = 1 to 2;

j = 1 to 2;

k = 0 to 5;

l = 1 to 14 for Cross 1; l = 1 to 24 for Cross 2;

m = 1 to 49 for Cross 1; m = 1 to 36 for Cross 2;

A_i = effect of the ith location;

R_{ij} = effect of the jth replication in the ith location;

L_k = effect of the kth locus class;

E_{kl} = effect of the lth enzyme class in the kth locus class;

G_{klm} = effect of the mth genotype in the lth enzyme class in the kth locus class;

$(AL)_{ik}$ = effect of the interaction of the ith location with the kth locus class;

$(AE)_{ikl}$ = effect of the interaction of the ith location with the lth enzyme class in the kth locus class;

$(AG)_{iklm}$ = effect of the interaction of the ith location with the mth genotype in the lth enzyme class in the kth locus class;

$(RL)_{ijk}$ = effect of the interaction of the kth locus class with the jth replication in the ith location;

$(RE)_{ijkl}$ = effect of the interaction of the lth enzyme class in the kth locus class with the jth replication in the ith location;

$(RG)_{ijklm}$ = effect of the interaction of the mth genotype in the lth enzyme class in the kth locus class with the jth replication in the ith location.

In the analysis of variance, the mean squares due to enzymes within loci, genotype within enzyme within loci, and their interactions with locations and replications within locations were each subdivided into six locus classes, 0 to 5.

The F test for significance of the mean squares for loci was tested with the location x loci mean squares. The significance of the enzyme within loci mean squares was tested using an approximate F test (Satterthwaite, 1946), where

$F'_{p,q}$ = (M1 + M5)/(M2 + M4) and

M1 = enzyme within loci mean square;

M2 = genotype within enzyme within loci mean square;

M4 = location x enzyme within loci mean square;

M5 = location x genotype within enzyme within loci mean square.

The appropriate degrees of freedom for the F' statistic were calculated according to Satterthwaite (1946) as follows:

$$p = (M1 + M5)^2/[(M1^2/f_1) + (M5^2/f_5)]$$

$$q = (M2 + M4)^2/[(M2^2/f_2) + (M4^2/f_4)]$$

where f_1, f_2, f_4, and f_5 are the degrees of freedom for the corresponding mean squares (Table 5). The significance of the genotype within enzyme within loci mean squares was tested against the location x genotype within enzyme within loci mean squares. The significance of the location mean squares and the entry mean squares was tested with the location x entry mean squares. The error mean squares were used to test the significance of the location x entry and the replications within locations mean squares. The significance of the mean squares for the interaction of locations with loci was tested with the replications within locations x loci mean squares. Likewise, the replications within locations x enzymes within loci mean squares were used to test the significance of the location x enzyme within loci mean squares, and the replications within locations x genotype within enzyme within loci mean squares were used to test the significance of the location x genotype within enzyme within loci mean squares.

Table 5. Analysis of variance for BC_2F_4-derived lines combined over locations

Sources of variation	Degrees of freedom
Location (A)	(a-1)
Replication/A (R/A)	(r-1)
Entry (V)	(v-1)
Loci (L)	(1-1)
Enzyme/Loci (E/L)	1(e-1)
E/L=0	(e_0-1)
E/L=1	(e_1-1)
E/L=2	(e_2-1)
E/L=3	(e_3-1)
E/L=4	(e_4-1)
E/L=5	(e_5-1)

Expectations of mean squares	Mean squares
$\sigma^2 + r\sigma^2_{AV} + rv\sigma^2_A$	
$\sigma^2 + v\sigma^2_{R/A}$	
$\sigma^2 + r\sigma^2_{AV} + ra\sigma^2_V$	
$eg\sigma^2_{R/AL} + reg\sigma^2_{AL} + ra(L)^2/(1-1)$	
$\sigma^2_{R/AG/E/L} + g\sigma^2_{R/AE/L} + rg\sigma^2_{AE/L} + ra\sigma^2_{G/E/L}$ + $rag(E/L)^2/[1(e-1)]$	M1
$\sigma^2_{R/AG/E/L=0} + g_0\sigma^2_{R/AE/L=0} + rg_0\sigma^2_{AE/L=0} + ra\sigma^2_{G/E/L=0}$ + $rag_0(E/L=0)^2/[1(e_0-1)]$	
$\sigma^2_{R/AG/E/L=1} + g_1\sigma^2_{R/AE/L=1} + rg_1\sigma^2_{AE/L=1} + ra\sigma^2_{G/E/L=1}$ + $rag_1(E/L=1)^2/[1(e_1-1)]$	
$\sigma^2_{R/AG/E/L=2} + g_2\sigma^2_{R/AE/L=2} + rg_2\sigma^2_{AE/L=2} + ra\sigma^2_{G/E/L=2}$ + $rag_2(E/L=2)^2/[1(e_2-1)]$	
$\sigma^2_{R/AG/E/L=3} + g_3\sigma^2_{R/AE/L=3} + rg_3\sigma^2_{AE/L=3} + ra\sigma^2_{G/E/L=3}$ + $rag_3(E/L=3)^2/[1(e_3-1)]$	
$\sigma^2_{R/AG/E/L=4} + g_4\sigma^2_{R/AE/L=4} + rg_4\sigma^2_{AE/L=4} + ra\sigma^2_{G/E/L=4}$ + $rag_4(E/L=4)^2/[1(e_4-1)]$	
$\sigma^2_{R/AG/E/L=5} + g_5\sigma^2_{R/AE/L=5} + rg_5\sigma^2_{AE/L=5} + ra\sigma^2_{G/E/L=5}$ + $rag_5(E/L=5)^2/[1(e_5-1)]$	

Table 5. Continued

Sources of variation	Degrees of freedom
Genotype/Enzyme/Loci (G/E/L)	$le(g-1)$
G/E/L=0	$e_0(g_0-1)$
G/E/L=1	$e_1(g_1-1)$
G/E/L=2	$e_2(g_2-1)$
G/E/L=3	$e_3(g_3-1)$
G/E/L=4	$e_4(g_4-1)$
G/E/L=5	$e_5(g_5-1)$
A X V	$(a-1)(v-1)$
A X L	$(a-1)(l-1)$
A X E/L	$l(a-1)(e-1)$
A X E/L=0	$(a-1)(e_0-1)$
A X E/L=1	$(a-1)(e_1-1)$
A X E/L=2	$(a-1)(e_2-1)$
A X E/L=3	$(a-1)(e_3-1)$
A X E/L=4	$(a-1)(e_4-1)$
A X E/L=5	$(a-1)(e_5-1)$

Expectations of mean squares	Mean squares
$\sigma^2_{R/AG/E/L} + ra\sigma^2_{G/E/L}$	M2
$\sigma^2_{R/AG/E/L=0} + ra\sigma^2_{G/E/L=0}$	
$\sigma^2_{R/AG/E/L=1} + ra\sigma^2_{G/E/L=1}$	
$\sigma^2_{R/AG/E/L=2} + ra\sigma^2_{G/E/L=2}$	
$\sigma^2_{R/AG/E/L=3} + ra\sigma^2_{G/E/L=3}$	
$\sigma^2_{R/AG/E/L=4} + ra\sigma^2_{G/E/L=4}$	
$\sigma^2_{R/AG/E/L=5} + ra\sigma^2_{G/E/L=5}$	
$\sigma^2 + r\sigma^2_{AV}$	
$eg\sigma^2_{R/AL} + reg\sigma^2_{AL}$	M3
$\sigma^2_{R/AG/E/L} + g\sigma^2_{R/AE/L} + rg\sigma^2_{AE/L}$	M4
$\sigma^2_{R/AG/E/L=0} + g_0\sigma^2_{R/AE/L=0} + rg_0\sigma^2_{AE/L=0}$	
$\sigma^2_{R/AG/E/L=1} + g_0\sigma^2_{R/AE/L=1} + rg_0\sigma^2_{AE/L=1}$	
$\sigma^2_{R/AG/E/L=2} + g_0\sigma^2_{R/AE/L=2} + rg_0\sigma^2_{AE/L=2}$	
$\sigma^2_{R/AG/E/L=3} + g_0\sigma^2_{R/AE/L=3} + rg_0\sigma^2_{AE/L=3}$	
$\sigma^2_{R/AG/E/L=4} + g_0\sigma^2_{R/AE/L=4} + rg_0\sigma^2_{AE/L=4}$	
$\sigma^2_{R/AG/E/L=5} + g_0\sigma^2_{R/AE/L=5} + rg_0\sigma^2_{AE/L=5}$	

Table 5. Continued

Sources of variation	Degrees of freedom
A X G/E/L	$1e(g-1)(a-1)$
A X G/E/L=0	$e_0(g_0-1)(a-1)$
A X G/E/L=1	$e_1(g_1-1)(a-1)$
A X G/E/L=2	$e_2(g_2-1)(a-1)$
A X G/E/L=3	$e_3(g_3-1)(a-1)$
A X G/E/L=4	$e_4(g_4-1)(a-1)$
A X G/E/L=5	$e_5(g_5-1)(a-1)$
Error (R/A X V)	$a(r-1)(v-1)$
R/A X L	$a(r-1)(1-1)$
R/A X E/L	$a1(r-1)(e-1)$
R/A X E/L=0	$a(r-1)(e_0-1)$
R/A X E/L=1	$a(r-1)(e_1-1)$
R/A X E/L=2	$a(r-1)(e_2-1)$
R/A X E/L=3	$a(r-1)(e_3-1)$
R/A X E/L=4	$a(r-1)(e_4-1)$
R/A X E/L=5	$a(r-1)(e_5-1)$

Expectations of mean squares	Mean squares
$\sigma^2_{R/AG/E/L} + r\sigma^2_{AG/E/L}$	M5
$\sigma^2_{R/AG/E/L=0} + r\sigma^2_{AG/E/L=0}$	
$\sigma^2_{R/AG/E/L=1} + r\sigma^2_{AG/E/L=1}$	
$\sigma^2_{R/AG/E/L=2} + r\sigma^2_{AG/E/L=2}$	
$\sigma^2_{R/AG/E/L=3} + r\sigma^2_{AG/E/L=3}$	
$\sigma^2_{R/AG/E/L=4} + r\sigma^2_{AG/E/L=4}$	
$\sigma^2_{R/AG/E/L=5} + r\sigma^2_{AG/E/L=5}$	
σ^2	
$eg\sigma^2_{R/AL}$	
$\sigma^2_{R/AG/E/L} + g\sigma^2_{R/AE/L}$	
$\sigma^2_{R/AG/E/L=0} + g_0\sigma^2_{R/AE/L=0}$	
$\sigma^2_{R/AG/E/L=1} + g_0\sigma^2_{R/AE/L=1}$	
$\sigma^2_{R/AG/E/L=2} + g_0\sigma^2_{R/AE/L=2}$	
$\sigma^2_{R/AG/E/L=3} + g_0\sigma^2_{R/AE/L=3}$	
$\sigma^2_{R/AG/E/L=4} + g_0\sigma^2_{R/AE/L=4}$	
$\sigma^2_{R/AG/E/L=5} + g_0\sigma^2_{R/AE/L=5}$	

Table 5. Continued

Sources of variation	Degrees of freedom
R/A X G/E/L	$ale(r-1)(g-1)$
R/A X G/E/L=0	$ae_0(r-1)(g_0-1)$
R/A X G/E/L=1	$ae_1(r-1)(g_1-1)$
R/A X G/E/L=2	$ae_2(r-1)(g_2-1)$
R/A X G/E/L=3	$ae_3(r-1)(g_3-1)$
R/A X G/E/L=4	$ae_4(r-1)(g_4-1)$
R/A X G/E/L=5	$ae_5(r-1)(g_5-1)$

Expectations of mean squares	Mean squares
$\sigma^2_{R/AG/E/L}$	
$\sigma^2_{R/AG/E/L=0}$	
$\sigma^2_{R/AG/E/L=1}$	
$\sigma^2_{R/AG/E/L=2}$	
$\sigma^2_{R/AG/E/L=3}$	
$\sigma^2_{R/AG/E/L=4}$	
$\sigma^2_{R/AG/E/L=5}$	

RESULTS

Analyses of variance for each location indicated highly significant ($P < 0.01$) differences among entries for maturity (MAT) and height (HT) in both crosses (Tables 6 and 7). Significant ($P < 0.05$) differences among entries for lodging (LDG), plant type (PLT), and vining (VNG) were observed only at the Ames location for Cross 2 (Table 7). Variation among locus classes (Loci), enzymes within locus classes (Enzyme/Loci), and lines (genotypes) within enzymes within loci were partitioned from the variation among all entries. Differences among locus classes were significant ($P < 0.05$) or highly significant ($P < 0.01$) in both crosses at each location, except for LDG, PLT, and VNG in Cross 2 at Burkey. Differences among enzymes within loci were significant ($P < 0.01$) for MAT and HT in both crosses at each location, but significant variation for LDG, PLT, and VNG was not detected at more than one location for either cross. There were significant ($P < 0.01$) differences among lines within enzymes within loci in both crosses at each location for all traits.

The analyses of variance combined across all environments indicated significant variation among entries in both crosses for all traits (Tables 8 and 9). In Cross 1, loci and genotypes within enzymes within loci were significantly different for all traits (Table 8). The significant differences among locus classes suggested that lines with different numbers of homozygous marker loci had significantly different phenotypic values for the traits. There were significant differences among enzymes within loci for all traits except LDG. For the 0-locus

Table 6. Analyses of variance for five traits of lines from Cross 1 at individual locations in 1986

Sources of variation	df	Mean squares	
		Ames	
		MAT	HT
Replications (R)	1	195**	2,293**
Entries (V)	282	154**	1,235**
Loci (L)	5	336**	9,011**
Enzymes/L (E/L)	25	752**	3,703**
E/L=0	0	0	0
E/L=1	5	1,014**	2,827**
E/L=2	13	757**	4,372**
E/L=3	5	682**	3,954**
E/L=4	2	233**	916
E/L=5	0	0	0
Genotypes/E/L (G/E/L)	252	92**	836**
G/E/L=0	48	109**	977**
G/E/L=1	86	109**	799**
G/E/L=2	74	82**	808**
G/E/L=3	31	53**	647
G/E/L=4	9	29**	1,129*
G/E/L=5	4	120**	1,236*
Error (RxV)	282	6	250
RxL	5	12	84
RxE/L	25	7	255
RxE/L=0	0	0	0
RxE/L=1	5	8	157
RxE/L=2	13	8	272
RxE/L=3	5	3	335
RxE/L=4	2	7	192
RxE/L=5	0	0	0
RxG/E/L	252	5	253
RxG/E/L=0	48	5	235
RxG/E/L=1	86	7	238
RxG/E/L=2	74	4	210
RxG/E/L=3	31	6	396
RxG/E/L=4	9	3	376
RxG/E/L=5	4	2	160
C.V. (%)		7.7	14.4

*, **Significant at the 0.05 and 0.01 probability levels, respectively.

Mean squares							
Ames			Burkey				
LDG	PLT	VNG	MAT	HT	LDG	PLT	VNG
9.11**	92.65**	43.00**	9	17,754**	0.24	0.93	7.01**
0.39	0.72	1.02	136**	943**	0.18	1.06	1.32
2.04**	4.12*	9.12**	319**	6,677**	0.75*	5.09**	7.47**
0.44	1.61	2.08*	3,268**	2,865**	0.19	1.59**	1.61
0	0	0	0	0	0	0	0
1.11*	2.16	1.66	1,002**	2,463*	0.19	2.80	2.18
0.34	1.96	2.76	589**	3,012**	0.23**	1.80	2.09**
0.23	0.85	1.37*	668**	2,668**	0.13	0.23	0.23
0.02	0.34	0.48	167**	3,400**	0.01	0.58	0.47
0	0	0	0	0	0	0	0
0.35**	0.57**	0.75**	81**	639**	0.16**	0.89**	1.16**
0.77**	0.90**	1.06**	103**	667**	0.36	1.03**	1.36**
0.28**	0.64**	0.85**	90**	659**	0.14	0.97*	1.15*
0.30**	0.50*	0.71**	82**	758**	0.11	0.79**	1.01**
0.14	0.19	0.35	37**	348	0.12**	0.57	1.09*
0.05	0.20	0.15	18**	146	0.07	1.37**	1.93*
0.06	0.10	0.10	66**	1,012*	0.01	0.40	0.85
0.14	0.42	0.41	4	210	0.11	0.53	0.60
0.10	0.66	0.13	5	160	0.10	0.37	0.23
0.09	0.80	0.79	4	206	0.06	0.77	0.47
0	0	0	0	0	0	0	0
0.15	0.66	0.93	9	269	0.12	1.19	0.68
0.09	1.06	1.00	4	153	0.03	0.50	0.30
0.05	0.51	0.38	1	336	0.09	1.29	0.77
0.02	0.18	0.20	1	63	0.03	0.24	0.25
0	0	0	0	0	0	0	0
0.15	0.38	0.38	5	211	0.11	0.51	0.62
0.29	0.52	0.42	4	143	0.25	0.54	0.59
0.15	0.36	0.31	4	259	0.10	0.58	0.67
0.09	0.31	0.39	5	210	0.08	0.45	0.58
0.09	0.42	0.54	5	239	0.05	0.48	0.59
0.05	0.34	0.34	2	77	0.09	0.22	0.48
0.08	0.10	0.10	2	127	0.07	0.60	1.35
8.3	15.0	16.6	7.7	13.0	7.2	17.2	21.6

Table 7. Analyses of variance for five traits of lines from Cross 2 at individual locations in 1986

Sources of variation	df	Mean squares	
		Ames	
		MAT	HT
Replications (R)	1	156**	2,521**
Entries (V)	621	209**	1,661**
Loci (L)	5	337**	6,524*
Enzymes/L (E/L)	64	874**	6,661**
E/L=0	0	0	0
E/L=1	7	1,342**	7,046**
E/L=2	20	894**	7,696**
E/L=3	23	865**	7,760**
E/L=4	10	683**	2,712**
E/L=5	4	492**	4,369**
Genotypes/E/L (G/E/L)	552	130**	1,037**
G/E/L=0	35	122**	1,488**
G/E/L=1	139	123**	1,097**
G/E/L=2	188	163**	1,063**
G/E/L=3	133	120**	1,002**
G/E/L=4	42	64**	681**
G/E/L=5	15	76**	425
Error (RxV)	621	7	180
RxL	5	9	779
RxE/L	64	6	161
RxE/L=0	0	0	0
RxE/L=1	7	6	108
RxE/L=2	20	3	185
RxE/L=3	23	5	156
RxE/L=4	10	11	163
RxE/L=5	4	8	160
RxG/E/L	552	7	177
RxG/E/L=0	35	4	132
RxG/E/L=1	139	7	131
RxG/E/L=2	188	6	198
RxG/E/L=3	133	7	197
RxG/E/L=4	42	7	142
RxG/E/L=5	15	6	353
C.V. (%)		10.6	14.2

*, **Significant at the 0.05 and 0.01 probability levels, respectively.

Mean squares							
Ames			Burkey				
LDG	PLT	VNG	MAT	HT	LDG	PLT	VNG
1.64*	50.64**	15.76**	1	3,027**	0.36	21.36**	5.02**
1.09*	2.28*	2.34*	182**	1,654**	0.95	1.15	1.67
9.59**	17.34**	16.36**	292**	4,503**	2.63	2.64	3.06
2.70**	6.97**	8.62**	721**	6,547**	1.81	1.51	5.79**
0	0	0	0	0	0	0	0
3.54**	9.93**	10.38**	934**	7,196**	2.84*	1.07	6.25*
4.05**	9.25**	10.69**	730**	7,661**	2.21**	1.60	6.51**
2.23**	5.06**	7.22**	721**	7,357**	1.38**	1.38	5.91**
0.90	2.45	4.95**	690**	2,996*	1.15	1.54	3.68
1.71*	12.73**	12.41**	385**	4,054**	2.02**	2.55	5.87**
0.83**	1.59**	1.49**	119**	1,061**	0.83**	1.10**	1.18**
1.36**	1.87**	1.65**	110**	1,199**	1.04*	1.54**	1.51**
0.81**	1.86**	1.65**	117**	1,131**	0.97**	1.08**	1.16**
0.89**	1.50**	1.44**	139**	1,119**	0.90**	1.06**	1.21**
0.76**	1.51**	1.51**	120**	970**	0.66**	0.97**	1.14**
0.55**	1.47**	1.24**	63**	954**	0.63**	1.27*	1.14**
0.36*	0.76*	0.72**	53**	463	0.25	1.49*	0.61
0.27	0.50	0.36	5	172	0.32	0.78	0.57
0.66	0.84	0.33	3	387	0.56	5.09	3.52
0.21	0.50	0.35	4	184	0.23	1.09	0.77
0	0	0	0	0	0	0	0
0.25	0.39	0.35	2	363	0.39	2.27	1.27
0.29	0.68	0.59	2	134	0.26	0.79	0.58
0.18	0.35	0.25	7	139	0.20	1.13	0.66
0.16	0.53	0.18	4	282	0.15	1.04	1.27
0.11	0.52	0.07	4	139	0.13	0.52	0.30
0.27	0.50	0.36	5	169	0.33	0.71	0.52
0.45	0.51	0.41	4	184	0.49	0.61	0.44
0.32	0.57	0.34	5	137	0.39	0.71	0.53
0.28	0.46	0.39	5	137	0.28	0.75	0.49
0.20	0.51	0.38	6	190	0.33	0.71	0.62
0.19	0.51	0.31	6	276	0.20	0.66	0.36
0.15	0.23	0.17	4	350	0.28	0.49	0.36
12.8	20.0	19.5	11.0	12.8	13.8	22.0	23.8

Table 8. Analyses of variance for five traits of lines from Cross 1 combined across two locations

Sources of variation	df	Mean squares				
		MAT	HT	LDG	PLT	VNG
Locations (A)	1	2,771.0**	872.0	1.50**	1.70	22.30**
Replications/A (R/A)	2	102.0**	10,024.0**	4.70**	46.80**	25.00**
Entries (V)	282	283.5**	1,791.8**	0.38**	1.27**	1.70**
Loci (L)	5	653.8**	14,599.6**	2.62**	8.52**	15.78**
Enzymes/Loci (E/L)	25	1,397.9**	5,844.7**	0.40	2.85**	3.08**
E/L=0	0	0	0	0	0	0
E/L=1	5	2,004.0**	4,602.4*	0.78	4.74**	3.32
E/L=2	13	1,337.8**	6,645.8**	0.43*	3.27**	4.29**
E/L=3	5	1,348.0**	6,152.8**	0.10	0.66	0.60
E/L=4	2	397.5**	3,473.0	0.05*	0.90	0.80
E/L=5	0	0	0	0	0	0
G/E/L	252	165.6**	1,131.6**	0.34**	0.97**	1.29**
G/E/L=0	48	205.7**	1,325.8**	0.90**	1.46**	1.93**
G/E/L=1	86	193.0**	1,132.6**	0.24**	1.09**	1.34**
G/E/L=2	74	157.5**	1,215.8**	0.22	0.75	1.09*
G/E/L=3	31	81.0**	615.4	0.12	0.48	0.82
G/E/L=4	9	41.3**	912.9	0.03	1.00	0.88
G/E/L=5	4	179.8**	1,716.5	0.05	0.43	0.75
AxV	282	6.8**	386.2**	0.18**	0.47**	0.63**
AxL	5	1.0	1,088.2**	0.16	0.68	0.80*
AxE/L	25	7.6	683.2**	0.23**	0.35	0.60
AxE/L=0	0	0	0	0	0	0
AxE/L=1	5	11.6	688.0	0.52*	0.22	0.52
AxE/L=2	13	8.7	738.7**	0.14*	0.42	0.55
AxE/L=3	5	2.4	469.8	0.24*	0.42	1.00
AxE/L=4	2	3.0	844.0	0	0.05	0.15
AxE/L=5	0	0	0	0	0	0

*, **Significant at the 0.05 and 0.01 probability levels, respectively.

Table 8. Continued

Sources of variation	df	Mean squares				
		MAT	HT	LDG	PLT	VNG
AxG/E/L	252	6.9**	342.8**	0.18**	0.48**	0.63**
AxG/E/L=0	48	6.3	318.8*	0.22	0.47	0.50
AxG/E/L=1	86	6.3	325.4*	0.18*	0.52	0.66*
AxG/E/L=2	74	7.2**	350.5**	0.19**	0.54*	0.63*
AxG/E/L=3	31	9.2*	379.6	0.13*	0.28	0.62
AxG/E/L=4	9	5.3	361.9	0.09	0.57	1.21*
AxG/E/L=5	4	6.3	531.3	0.03	0.08	0.20
Error (R/AxV)	564	5.0	229.8	0.13	0.47	0.51
R/AxL	10	8.3	12.2	0.10	0.51	0.18
R/AxE/L	50	5.3	230.5	0.07	0.79	0.63
R/AxE/L=0	0	0	0	0	0	0
R/AxE/L=1	10	8.3	212.8	0.13	0.92	0.80
R/AxE/L=2	26	5.7	212.7	0.06	0.78	0.65
R/AxE/L=3	10	2.0	335.6	0.07	0.90	0.57
R/AxE/L=4	4	4.0	127.5	0.03	0.20	0.23
R/AxE/L=5	0	0	0	0	0	0
R/AxG/E/L	504	4.9	231.9	0.13	0.44	0.50
R/AxG/E/L=0	96	4.5	189.0	0.27	0.53	0.50
R/AxG/E/L=1	172	5.5	248.6	0.13	0.47	0.49
R/AxG/E/L=2	148	4.6	209.9	0.09	0.38	0.48
R/AxG/E/L=3	62	5.4	317.3	0.07	0.45	0.56
R/AxG/E/L=4	18	2.7	226.8	0.07	0.28	0.41
R/AxG/E/L=5	8	2.3	143.5	0.08	0.35	0.73
C.V. (%)		7.7	13.7	7.7	16.1	19.1

Table 9. Analyses of variance for five traits of lines from Cross 2 combined across two locations

Sources of variation	df	Mean squares				
		MAT	HT	LDG	PLT	VNG
Locations (A)	1	9,968**	43,153**	4.0**	147.0**	4.0**
Replications/A (R/A)	2	78**	2,275**	1.0*	36.0**	10.5**
Entries (V)	621	382**	3,061**	1.7**	2.3**	3.4**
Loci (L)	5	620**	10,898**	10.8*	12.8	15.6
Enzymes/Loci (E/L)	64	1,580**	12,970**	4.1**	6.2**	13.7**
E/L=0	0	0	0	0	0	0
E/L=1	7	2,249**	13,846**	6.1**	8.3	16.1**
E/L=2	20	1,611**	15,115**	5.7**	7.4	16.3**
E/L=3	23	1,568**	14,847**	3.4**	4.9*	12.7**
E/L=4	10	1,364**	5,616**	1.7	2.6	7.7**
E/L=5	4	867**	8,300**	3.5*	12.5	17.3**
G/E/L	552	240**	1,841**	1.3**	1.7**	2.1**
G/E/L=0	35	227**	2,413**	1.9**	2.0	2.6**
G/E/L=1	139	233**	2,026**	1.4**	2.1**	2.3**
G/E/L=2	188	292**	1,957**	1.5**	1.7**	2.1**
G/E/L=3	133	232**	1,634**	1.1**	1.6**	2.1**
G/E/L=4	42	116**	1,332**	0.8*	1.2	1.2
G/E/L=5	15	123**	582	0.3	0.9	0.7
AxV	621	9.3**	254**	0.4**	1.2**	0.6**
AxL	5	9.4	129	1.6	7.2**	3.8
AxE/L	64	15.4**	238*	0.4**	2.3**	0.7
AxE/L=0	0	0	0	0	0	0
AxE/L=1	7	27.6**	396	0.3	2.7	0.6
AxE/L=2	20	13.4**	242	0.6	3.5**	1.0
AxE/L=3	23	17.2**	270	0.2	1.5*	0.4
AxE/L=4	10	9.0	92	0.4	1.4	0.9
AxE/L=5	4	9.8	124	0.3	3.0*	1.0**

*, **Significant at the 0.05 and 0.01 probability levels, respectively.

Table 9. Continued

Sources of variation	df	Mean squares				
		MAT	HT	LDG	PLT	VNG
AxG/E/L	552	8.5**	258**	0.3**	1.0**	0.6**
AxG/E/L=0	35	5.6	273*	0.5	1.4**	0.6
AxG/E/L=1	139	7.4**	202**	0.4	0.8**	0.5*
AxG/E/L=2	188	9.4**	225**	0.3**	0.9**	0.6**
AxG/E/L=3	133	8.8**	337**	0.3	0.9**	0.5
AxG/E/L=4	42	10.6*	303	0.4**	1.6**	1.1**
AxG/E/L=5	15	6.5	306	0.3	1.3**	0.7*
Error (R/AxV)	1242	5.8	176	0.3	0.6	0.5
R/AxL	10	6.2	583	0.6	0.3	1.9
R/AxE/L	128	5.1	173	0.2	0.8	0.6
R/AxE/L=0	0	0	0	0	0	0
R/AxE/L=1	14	4.0	235	0.3	1.4	0.8
R/AxE/L=2	40	2.8	395	0.3	0.7	0.6
R/AxE/L=3	46	6.1	147	0.2	0.7	0.5
R/AxE/L=4	20	7.6	223	0.2	0.8	0.8
R/AxE/L=5	8	5.9	150	0.1	0.5	0.1
R/AxG/E/L	1104	5.9	173	0.3	0.6	0.4
R/AxG/E/L=0	70	4.0	158	0.5	0.6	0.4
R/AxG/E/L=1	278	5.8	134	0.4	0.6	0.4
R/AxG/E/L=2	376	5.7	168	0.3	0.6	0.4
R/AxG/E/L=3	266	6.4	193	0.3	0.6	0.5
R/AxG/E/L=4	84	6.6	209	0.2	0.6	0.3
R/AxG/E/L=5	30	5.4	352	0.2	0.4	0.3
C.V. (%)		10.8	13.5	13.4	21.2	21.8

class (random BC_2F_4-derived lines that had retained no alleles from G. soja at any of the isozyme marker loci), entries were significantly different for all traits. The same occurred for the 1-locus class. For the 2-locus class, however, only MAT, HT, and VNG showed significant differences among entries. Genotypes within enzymes in the 3-, 4-, and 5-locus classes were different only for MAT. Differences among enzymes within the 1-locus class were significant for MAT, PLT, and HT, indicating the possibility of specific associations between particular enzyme loci and each of these traits. Significant differences among enzyme combinations in the 2-locus class for all traits suggested possible epistatic interactions between the marker loci or the genes linked to them that affect the quantitative traits. Only MAT and HT showed significantly different values among enzymes in the 3-locus class, and MAT and LDG in the 4-locus class. Only one 5-locus enzyme combination was present in the 5-locus class for Cross 1, so no comparisons could be made. In Cross 2, enzymes within loci and genotypes within enzymes within loci were different for all traits (Table 9). Variation among loci was significant for MAT, HT, and LDG, but not PLT and VNG. Significant differences among enzymes within every locus class were detected for MAT, HT, and VNG. For LDG, differences among enzymes were observed in the 1-, 2-, 3-, and 5-locus classes, and for PLT only in the 3-locus class. Variation among genotypes within enzyme classes was significant for all traits in every locus class, except HT, LDG, PLT, and VNG in the 5-locus class, PLT and VNG in the 4-locus class, and PLT in the 0-locus class.

Locations were significantly different for MAT, LDG, and VNG, but not HT and PLT in Cross 1 (Table 8). In Cross 2, locations differed significantly for all traits (Table 9). In both crosses there were significant location x entry interactions for all traits. Location x loci interactions were observed for HT and VNG in Cross 1, and for PLT in Cross 2. Values for enzymes within loci were significantly different between locations for HT and LDG in Cross 1, but not MAT, PLT and VNG. In Cross 2, the location x enzymes within loci interactions were significant for all traits except VNG (Table 9).

The coefficients of variation for each trait were larger for Cross 2 than for Cross 1 (Tables 6 through 9). For each cross, the coefficients for each trait were similar between individual locations and in the combined analysis. The coefficients of variation for PLT and VNG were always higher than for other traits in both crosses, and those for MAT were lowest.

One of the objectives of this study was to examine the relationships between agronomic performance of BC_2F_4-derived lines and the numbers of isozyme loci that were homozygous for alleles from G. soja. On the average, the second backcross population is expected to contain 12.5% donor germplasm. Glycine soja was used as the donor and G. max as the recurrent parent in these crosses. A relationship between numbers of loci with G. soja alleles and values for the quantitative traits would support the hypothesis that selection for G. soja alleles at marker loci resulted in the retention of a greater than average percentage of G. soja germplasm through linkage with the marker loci that were retained, and at least some of those linked genes affected

the quantitative traits under evaluation.

For every trait except MAT, an increase in the numbers of isozyme marker loci that were homozygous for G. soja alleles resulted in a change in the phenotype toward the G. soja parent in both crosses (Figures 1 through 5). For Cross 1, MAT showed no distinctive trends, but the mean maturities for the 3-, 4-, and 5-locus classes were later than either parent (Table 10). Mean HT increased with each additional marker locus until the 4- and 5-locus classes, which equalled the height of PI 326581. Lodging score increased up to the 2-locus class, which was not different from the 5-locus class. There was an increase for PLT toward the G. soja parent up to the 3-locus class and for VNG up to the 4-locus class. For Cross 2, MAT showed no distinctive trends, but the mean maturities for the 0-, 1-, 2-, and 4-locus classes were earlier than either parent (Table 11). Height increased toward the G. soja parent from the 0- to the 5-locus class, with a decrease in the 4-locus class. The mean scores for LDG and VNG increased up to the 2-locus class. The PLT scores increased toward the G. soja parent up to the 3-locus class, where the values were not different from the 5-locus class.

For both crosses, the mean MAT for lines in all locus classes at Burkey was four days less than at Ames (Tables 12 and 13). For Cross 1, mean HT was similar for both locations, except for the 5-locus class (Table 12). Lodging was slightly greater at Burkey, while PLT and VNG were greater at Ames. The G. max parent was taller at Burkey than at Ames, while the G. soja parent was taller at Ames. The response of the 5-locus class for HT was similar to the G. soja parent. For both

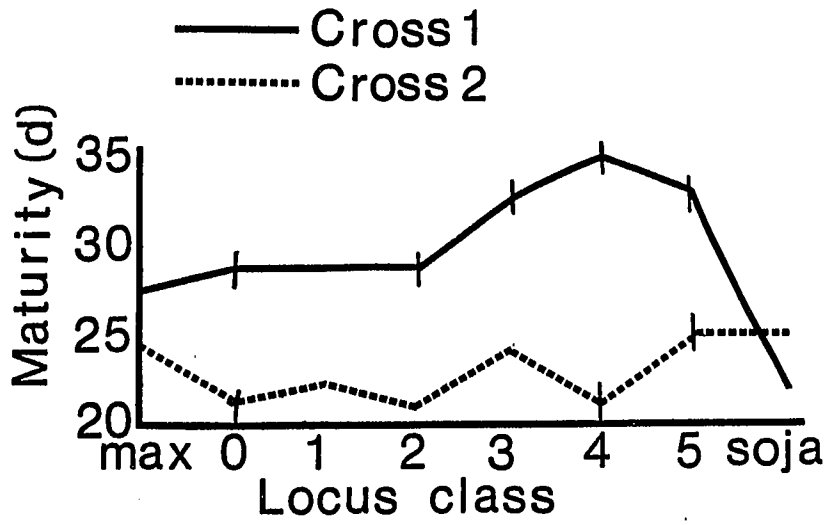

Figure 1. Mean maturity for the G. max and G. soja parents and the BC_2F_4-derived lines with different numbers of isozyme loci homozygous for G. soja alleles. (The vertical lines represent the standard errors of the means.)

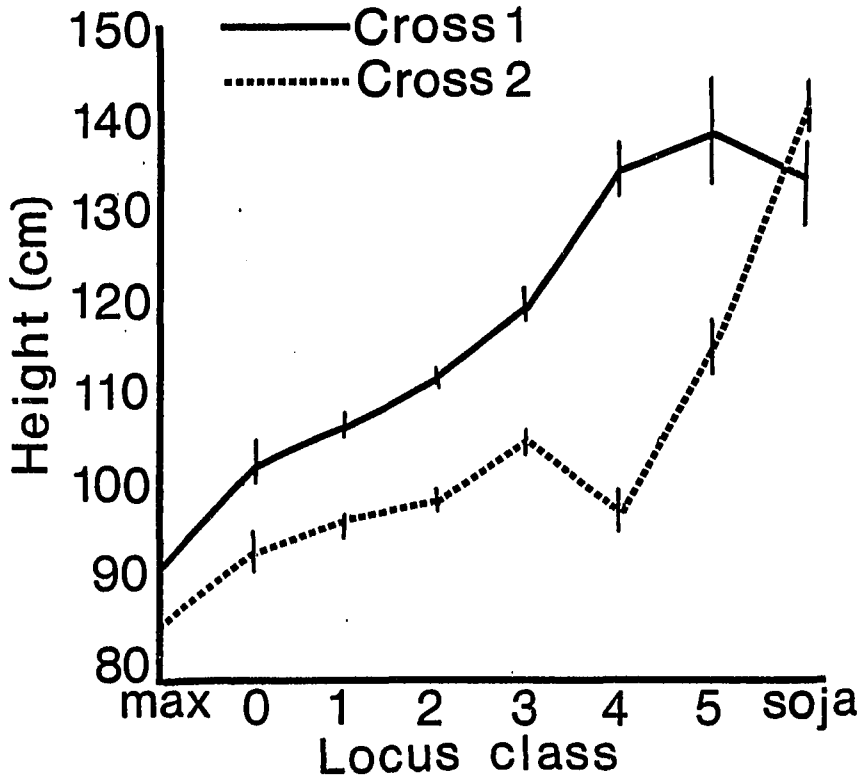

Figure 2. Mean height for the G. max and G. soja parents and the BC_2F_4-derived lines with different numbers of isozyme loci homozygous for G. soja alleles. (The vertical lines represent the standard errors of the means.)

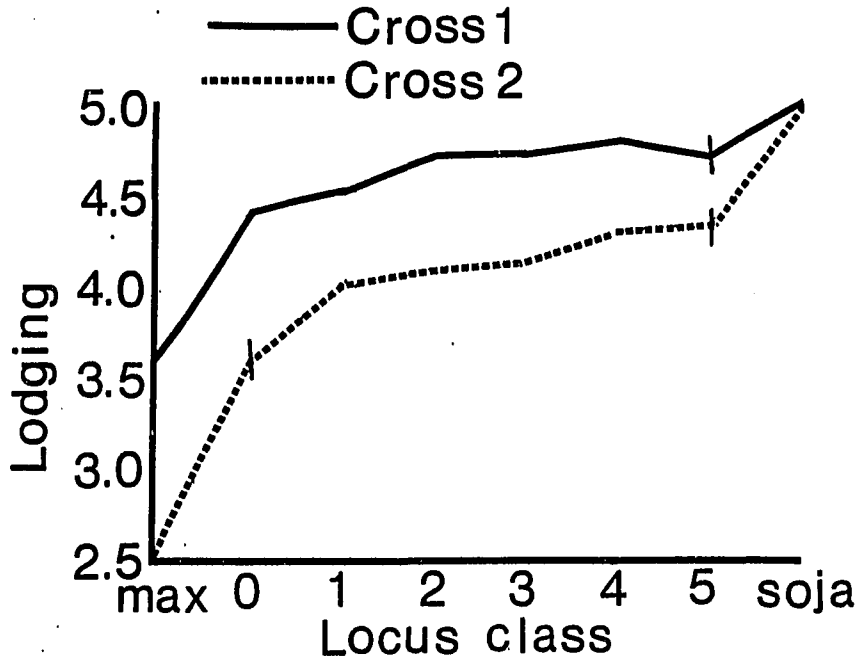

Figure 3. Mean lodging score for the G. max and G. soja parents and the BC_2F_4-derived lines with different numbers of isozyme loci homozygous for G. soja alleles. (The vertical lines represent the standard errors of the means.)

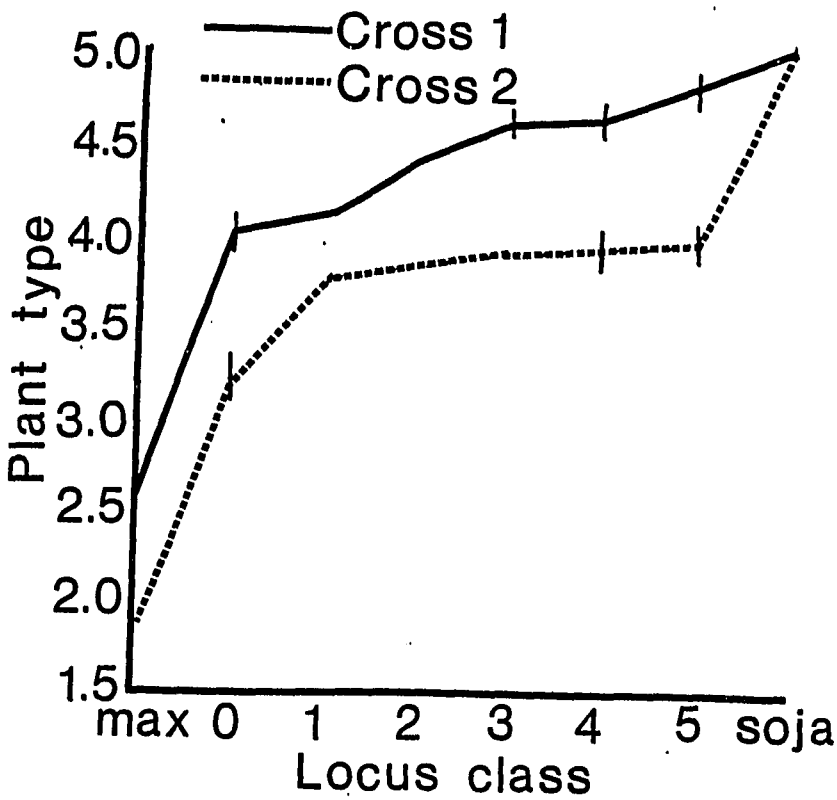

Figure 4. Mean plant type score for the G. max and G. soja parents and the BC_2F_4-derived lines with different numbers of isozyme loci homozygous for G. soja alleles. (The vertical lines represent the standard errors of the means.)

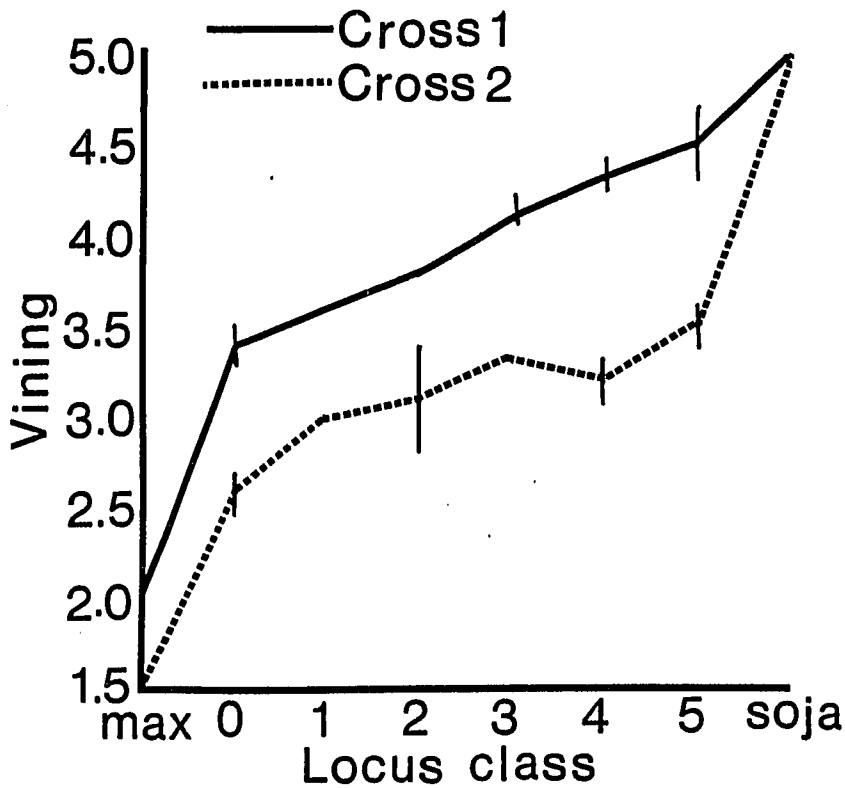

Figure 5. Mean vining score for the G. max and G. soja parents and the BC_2F_4-derived lines with different numbers of isozyme loci homozygous for G. soja alleles. (The vertical lines represent the standard errors of the means.)

Table 10. Means and standard errors for each locus class and the parents for Cross 1 averaged over two locations

Locus class[a]	Trait				
	MAT	HT	LDG	PLT	VNG
0	28 ± 1	102 ± 2	4.4 ± 0.0	4.0 ± 0.1	3.4 ± 0.1
1	28 ± 0	106 ± 1	4.5 ± 0.0	4.1 ± 0.0	3.6 ± 0.0
2	28 ± 1	111 ± 1	4.7 ± 0.0	4.4 ± 0.0	3.8 ± 0.0
3	32 ± 1	119 ± 2	4.7 ± 0.0	4.6 ± 0.1	4.1 ± 0.1
4	34 ± 1	134 ± 3	4.8 ± 0.0	4.6 ± 0.1	4.3 ± 0.1
5	32 ± 1	138 ± 6	4.7 ± 0.1	4.8 ± 0.1	4.5 ± 0.2
PI 326581	21 ± 0	133 ± 5	5.0 ± 0.0	5.0 ± 0.0	5.0 ± 0.0
A80-244036	27 ± 0	90 ± 1	3.6 ± 0.1	2.5 ± 0.2	2.0 ± 0.1

[a]The numbers of isozyme marker loci that are homozygous for *G. soja* alleles.

Table 11. Means and standard errors for each locus class and the parents of Cross 2 averaged over two locations

Locus class[a]	Trait				
	MAT	HT	LDG	PLT	VNG
0	21 ± 1	92 ± 2	3.6 ± 0.1	3.2 ± 0.1	2.6 ± 0.1
1	22 ± 0	95 ± 1	4.0 ± 0.0	3.7 ± 0.0	3.0 ± 0.0
2	21 ± 0	97 ± 1	4.1 ± 0.0	3.8 ± 0.0	3.1 ± 0.3
3	24 ± 0	104 ± 1	4.1 ± 0.0	3.9 ± 0.0	3.3 ± 0.0
4	21 ± 1	96 ± 2	4.3 ± 0.0	3.9 ± 0.1	3.2 ± 0.1
5	25 ± 1	114 ± 3	4.3 ± 0.1	3.9 ± 0.1	3.5 ± 0.1
PI 342618A	25 ± 0	141 ± 2	5.0 ± 0.0	5.0 ± 0.0	5.0 ± 0.0
A81-157007	24 ± 0	85 ± 1	2.5 ± 0.1	1.8 ± 0.1	1.5 ± 0.1

[a]The numbers of isozyme marker loci that are homozygous for *G. soja* alleles.

Table 12. Means and standard errors for each locus class and the parents for Cross 1 at individual locations

Locus class[a]	Trait				
	Ames				
	MAT	HT	LDG	PLT	VNG
0	29 ± 1	102 ± 3	4.3 ± 0.1	4.0 ± 0.1	3.5 ± 0.1
1	30 ± 1	105 ± 2	4.5 ± 0.0	4.3 ± 0.1	3.8 ± 0.1
2	30 ± 1	109 ± 2	4.6 ± 0.0	4.3 ± 0.1	3.9 ± 0.1
3	33 ± 1	118 ± 3	4.7 ± 0.0	4.6 ± 0.1	4.3 ± 0.1
4	36 ± 1	131 ± 5	4.8 ± 0.0	4.7 ± 0.1	4.3 ± 0.1
5	34 ± 2	153 ± 8	4.8 ± 0.1	4.9 ± 0.1	4.9 ± 0.1
Mean[b]	31 ± 0	109 ± 1	4.5 ± 0.0	4.3 ± 0.0	3.9 ± 0.0
PI 326581	22 ± 0	140 ± 8	5.0 ± 0.0	5.0 ± 0.0	5.0 ± 0.0
A80-244036	30 ± 0	84 ± 2	3.5 ± 0.2	2.2 ± 0.2	1.9 ± 0.2

[a]The numbers of isozyme marker loci that are homozygous for *G. soja* alleles.

[b]Average for BC_2F_4-derived lines in all locus classes.

Trait				
Burkey				
MAT	HT	LDG	PLT	VNG
26 ± 1	103 ± 2	4.5 ± 0.1	4.1 ± 0.1	3.3 ± 0.1
27 ± 1	107 ± 2	4.6 ± 0.0	4.0 ± 0.1	3.4 ± 0.1
27 ± 1	112 ± 2	4.7 ± 0.0	4.4 ± 0.1	3.7 ± 0.1
30 ± 1	120 ± 3	4.7 ± 0.0	4.6 ± 0.1	4.0 ± 0.1
33 ± 1	137 ± 4	4.8 ± 0.1	4.5 ± 0.2	4.2 ± 0.2
31 ± 2	123 ± 7	4.7 ± 0.1	4.7 ± 0.2	4.1 ± 0.3
27 ± 0	111 ± 1	4.6 ± 0.0	4.2 ± 0.0	3.6 ± 0.0
21 ± 0	125 ± 5	5.0 ± 0.0	5.0 ± 0.0	5.0 ± 0.0
25 ± 0	95 ± 1	3.8 ± 0.1	2.7 ± 0.2	2.2 ± 0.2

Table 13. Means and standard errors for each locus class and the parents for Cross 2 at individual locations

Locus class[a]	Trait				
	Ames				
	MAT	HT	LDG	PLT	VNG
0	24 ± 1	86 ± 3	3.5 ± 0.1	2.8 ± 0.1	2.4 ± 0.1
1	24 ± 1	91 ± 2	3.9 ± 0.0	3.3 ± 0.1	2.8 ± 0.1
2	23 ± 1	92 ± 2	4.0 ± 0.0	3.6 ± 0.1	3.1 ± 0.1
3	26 ± 1	100 ± 2	4.1 ± 0.0	3.7 ± 0.1	3.3 ± 0.1
4	23 ± 1	92 ± 2	4.4 ± 0.1	3.9 ± 0.1	3.4 ± 0.1
5	28 ± 1	111 ± 4	4.4 ± 0.1	3.8 ± 0.2	3.5 ± 0.2
Mean[b]	24 ± 0	94 ± 1	4.0 ± 0.0	3.5 ± 0.0	3.1 ± 0.0
PI 342618A	26 ± 0	146 ± 2	5.0 ± 0.0	5.0 ± 0.0	5.0 ± 0.0
A81-157007	27 ± 0	81 ± 1	2.5 ± 0.1	1.7 ± 0.1	1.5 ± 0.1

[a]The numbers of isozyme marker loci that are homozygous for *G. soja* alleles.

[b]Average for BC_2F_4-derived lines in all locus classes.

Trait				
Burkey				
MAT	HT	LDG	PLT	VNG
19 ± 1	97 ± 3	3.7 ± 0.1	3.7 ± 0.1	2.8 ± 0.1
20 ± 1	100 ± 2	4.1 ± 0.0	4.1 ± 0.1	3.1 ± 0.1
19 ± 0	101 ± 2	4.1 ± 0.0	4.1 ± 0.0	3.2 ± 0.1
22 ± 1	107 ± 2	4.2 ± 0.0	4.0 ± 0.1	3.3 ± 0.1
19 ± 1	99 ± 3	4.2 ± 0.1	4.0 ± 0.1	3.1 ± 0.1
23 ± 1	117 ± 4	4.2 ± 0.1	3.9 ± 0.2	3.4 ± 0.2
20 ± 0	102 ± 1	4.1 ± 0.0	4.0 ± 0.0	3.2 ± 0.0
24 ± 0	135 ± 3	5.0 ± 0.0	5.0 ± 0.0	5.0 ± 0.0
22 ± 0	88 ± 1	2.4 ± 0.1	1.9 ± 0.1	1.5 ± 0.1

parents, LDG, PLT, and VNG were similar at both locations. For Cross 2, the mean HT for each locus class and for the G. max parent, A81-157007, was greater at Burkey, but PI 342618A was taller at Ames (Table 13). The BC_2F_4-derived lines in each locus class behaved similarly across locations for LDG and VNG, but for PLT the 0-, 1-, 2-, and 3-locus classes at Ames had lower scores than at Burkey. For both parents, LDG, PLT, and VNG were similar at both locations.

A second objective of this research was to determine if specific marker loci or genes linked to them affected quantitative traits. Such an association between marker loci and genes that affect quantitative characters would be valuable to identify regions of the genome that have larger effects on important agronomic traits. To be most useful, the associations should be stable within and across environments and across populations. The applicability of specific marker locus/quantitative trait associations to different populations, however, is limited by the parental genotypes and the methods used to develop the populations.

Associations were found between specific enzyme locus genotypes and each of the quantitative traits that was measured. For both crosses, the effects of particular enzyme-locus genotypes were observed at both locations (Tables 14 through 22). The effects observed for individual marker loci and for the multilocus genotypes at each location were similar to the effects combined across locations (Tables 23 through 32). Discussion of the association of isozyme genotypes and quantitative traits will refer to the results combined across locations (Tables 23 through 32).

Table 14. Means and standard errors for each enzyme genotype in the 1-locus class for Cross 1 at individual locations

Enzyme locus genotype[a]	Trait				
	Ames				
	MAT	HT	LDG	PLT	VNG
0	29 ± 1	102 ± 3	4.3 ± 0.1	4.0 ± 0.1	3.5 ± 0.1
1	26 ± 1	112 ± 5	4.1 ± 0.2	3.6 ± 0.3	3.4 ± 0.2
2	26 ± 1	92 ± 4	4.1 ± 0.1	4.1 ± 0.2	3.5 ± 0.2
3	29 ± 1	102 ± 5	4.6 ± 0.1	4.2 ± 0.2	3.6 ± 0.2
4	39 ± 1	119 ± 3	4.6 ± 0.1	4.6 ± 0.1	4.1 ± 0.1
5	30 ± 2	104 ± 4	4.4 ± 0.1	4.1 ± 0.2	3.7 ± 0.2
6	26 ± 1	102 ± 3	4.5 ± 0.1	4.2 ± 0.1	3.7 ± 0.1

[a]0 = none of the isozyme loci has *G. soja* alleles; 1 = homozygous for the *Aco2-a* allele; 2 = homozygous for the *Idh2-a* allele; 3 = homozygous for the *Ap-c* allele; 4 = homozygous for the *Pgm1-a* allele; 5 = homozygous for the *Pgm2-b* allele; 6 = homozygous for the *Pgi-a* allele.

Trait				
Burkey				
MAT	HT	LDG	PLT	VNG
26 ± 1	103 ± 2	4.5 ± 0.1	4.1 ± 0.1	3.3 ± 0.1
21 ± 0	132 ± 7	4.3 ± 0.2	3.1 ± 0.3	2.9 ± 0.2
24 ± 1	93 ± 5	4.6 ± 0.1	4.1 ± 0.2	3.5 ± 0.2
27 ± 1	110 ± 3	4.6 ± 0.1	4.1 ± 0.2	3.4 ± 0.2
35 ± 1	113 ± 4	4.6 ± 0.1	4.4 ± 0.1	3.7 ± 0.1
28 ± 2	107 ± 5	4.5 ± 0.1	3.9 ± 0.2	3.1 ± 0.2
22 ± 1	103 ± 2	4.6 ± 0.0	3.9 ± 0.1	3.3 ± 0.1

Table 15. Means and standard errors for each enzyme genotype in the 2-locus class for Cross 1 at individual locations

Enzyme locus genotype[a]	Trait				
	Ames				
	MAT	HT	LDG	PLT	VNG
0	29 ± 1	102 ± 3	4.3 ± 0.1	4.0 ± 0.1	3.5 ± 0.1
12	25 ± 1	105 ± 6	4.7 ± 0.1	4.6 ± 0.1	4.4 ± 0.2
13	30 ± 2	116 ± 6	4.4 ± 0.2	4.3 ± 0.2	3.8 ± 0.2
14	46 ± 2	146 ± 8	4.9 ± 0.1	5.0 ± 0.0	4.8 ± 0.2
15	31 ± 1	144 ± 19	4.7 ± 0.2	5.0 ± 0.0	4.8 ± 0.3
16	21 ± 3	101 ± 5	4.6 ± 0.1	4.1 ± 0.2	3.6 ± 0.2
23	26 ± 2	103 ± 13	4.4 ± 0.2	4.3 ± 0.3	3.8 ± 0.3
24	29 ± 2	102 ± 7	4.4 ± 0.2	4.0 ± 0.3	3.6 ± 0.3
25	30 ± 0	113 ± 4	4.9 ± 0.1	4.2 ± 0.2	4.0 ± 0.2
26	25 ± 1	82 ± 3	4.6 ± 0.1	4.1 ± 0.2	3.4 ± 0.2
35	22 ± 1	85 ± 3	4.5 ± 0.1	3.5 ± 0.5	3.0 ± 0.5
36	23 ± 1	91 ± 7	4.6 ± 0.2	4.1 ± 0.3	3.8 ± 0.3
45	43 ± 1	130 ± 5	4.8 ± 0.1	4.8 ± 0.1	4.1 ± 0.2
46	41 ± 1	134 ± 5	4.9 ± 0.1	4.9 ± 0.1	4.7 ± 0.1
56	27 ± 2	102 ± 5	4.7 ± 0.1	4.3 ± 0.2	3.7 ± 0.2

[a]Each digit in the enzyme genotype indicates a locus that is homozygous for G. soja alleles. Refer to Table 14 for enzyme locus genotypes.

Trait				
Burkey				
MAT	HT	LDG	PLT	VNG
26 ± 1	103 ± 2	4.5 ± 0.1	4.1 ± 0.1	3.3 ± 0.1
23 ± 1	107 ± 8	4.7 ± 0.1	4.8 ± 0.2	3.9 ± 0.2
28 ± 2	123 ± 6	4.6 ± 0.1	4.3 ± 0.2	3.6 ± 0.2
41 ± 2	157 ± 7	4.7 ± 0.1	4.9 ± 0.1	3.8 ± 0.3
30 ± 2	124 ± 4	4.9 ± 0.1	5.0 ± 0.0	4.5 ± 0.3
18 ± 3	106 ± 6	4.5 ± 0.1	3.9 ± 0.2	3.2 ± 0.2
23 ± 1	85 ± 4	4.7 ± 0.1	4.5 ± 0.3	4.0 ± 0.3
28 ± 2	107 ± 7	4.3 ± 0.1	3.5 ± 0.3	3.0 ± 0.2
27 ± 0	120 ± 3	4.6 ± 0.1	4.3 ± 0.3	3.5 ± 0.3
22 ± 1	97 ± 5	4.7 ± 0.1	4.6 ± 0.2	3.6 ± 0.2
19 ± 1	92 ± 6	4.6 ± 0.1	3.9 ± 0.4	3.4 ± 0.4
20 ± 1	104 ± 8	4.7 ± 0.1	4.0 ± 0.3	3.3 ± 0.3
38 ± 1	129 ± 3	4.7 ± 0.1	4.4 ± 0.2	3.7 ± 0.2
35 ± 1	115 ± 6	4.9 ± 0.1	4.9 ± 0.1	4.4 ± 0.2
24 ± 2	113 ± 4	4.8 ± 0.1	4.3 ± 0.2	3.8 ± 0.2

Table 16. Means and standard errors for each enzyme genotype in the 3-locus class for Cross 1 at individual locations

Enzyme locus genotype[a]	Trait				
	Ames				
	MAT	HT	LDG	PLT	VNG
0	29 ± 1	102 ± 3	4.3 ± 0.1	4.0 ± 0.1	3.5 ± 0.1
126	27 ± 1	100 ± 6	4.8 ± 0.1	4.6 ± 0.2	4.5 ± 0.2
134	42 ± 1	133 ± 6	4.8 ± 0.1	4.9 ± 0.1	4.5 ± 0.4
135	29 ± 1	127 ± 10	4.5 ± 0.1	4.4 ± 0.2	4.2 ± 0.2
136	31 ± 2	122 ± 6	4.8 ± 0.1	4.3 ± 0.2	4.1 ± 0.2
146	40 ± 1	127 ± 5	4.7 ± 0.1	4.8 ± 0.1	4.4 ± 0.2
156	21 ± 1	81 ± 5	4.5 ± 0.2	4.3 ± 0.3	3.5 ± 0.3

[a]Each digit in the enzyme genotype indicates a locus that is homozygous for *G. soja* alleles. Refer to Table 14 for enzyme locus genotypes.

Trait				
Burkey				
MAT	HT	LDG	PLT	VNG
26 ± 1	103 ± 2	4.5 ± 0.1	4.1 ± 0.1	3.3 ± 0.1
23 ± 1	93 ± 3	4.8 ± 0.1	4.5 ± 0.2	4.1 ± 0.3
39 ± 1	133 ± 6	4.6 ± 0.1	4.4 ± 0.2	3.8 ± 0.2
27 ± 1	131 ± 4	4.7 ± 0.1	4.6 ± 0.2	4.1 ± 0.3
28 ± 2	121 ± 5	4.7 ± 0.1	4.6 ± 0.2	3.9 ± 0.2
36 ± 1	125 ± 6	4.7 ± 0.1	4.8 ± 0.2	4.0 ± 0.2
19 ± 1	104 ± 5	4.9 ± 0.1	4.4 ± 0.3	4.1 ± 0.3

Table 17. Means and standard errors for each enzyme genotype in the 4- and 5-locus classes for Cross 1 at individual locations

Enzyme locus genotype[a]	Trait				
	Ames				
	MAT	HT	LDG	PLT	VNG
0	29 ± 1	102 ± 3	4.3 ± 0.1	4.0 ± 0.1	3.5 ± 0.1
1345	39 ± 2	138 ± 7	4.7 ± 0.1	4.9 ± 0.1	4.5 ± 0.2
1346	39 ± 1	135 ± 7	4.8 ± 0.1	4.6 ± 0.2	4.4 ± 0.2
1356	29 ± 1	116 ± 15	4.8 ± 0.1	4.5 ± 0.3	4.0 ± 0.3
13456	34 ± 2	153 ± 8	4.8 ± 0.1	4.9 ± 0.1	4.9 ± 0.1

[a]Each digit in the enzyme genotype indicates a locus that is homozygous for *G. soja* alleles. Refer to Table 14 for enzyme locus genotype.

Trait				
Burkey				
MAT	HT	LDG	PLT	VNG
26 ± 1	103 ± 2	4.5 ± 0.1	4.1 ± 0.1	3.3 ± 0.1
35 ± 1	136 ± 4	4.8 ± 0.1	4.8 ± 0.2	4.4 ± 0.2
35 ± 1	157 ± 5	4.8 ± 0.1	4.4 ± 0.3	4.0 ± 0.4
26 ± 2	113 ± 6	4.8 ± 0.1	4.3 ± 0.4	4.0 ± 0.5
31 ± 2	123 ± 7	4.7 ± 0.1	4.7 ± 0.2	4.1 ± 0.3

Table 18. Means and standard errors for each enzyme genotype in the 1-locus class for Cross 2 at individual locations

Enzyme locus genotype[a]	Trait				
	Ames				
	MAT	HT	LDG	PLT	VNG
0	24 ± 1	86 ± 3	3.5 ± 0.1	2.8 ± 0.1	2.4 ± 0.1
1	33 ± 2	117 ± 7	4.5 ± 0.1	4.3 ± 0.2	4.0 ± 0.2
2	27 ± 1	93 ± 3	3.8 ± 0.1	3.2 ± 0.1	2.8 ± 0.1
3	31 ± 2	115 ± 4	4.4 ± 0.1	4.2 ± 0.2	3.7 ± 0.2
4	15 ± 1	78 ± 3	3.7 ± 0.1	3.0 ± 0.1	2.3 ± 0.1
5	14 ± 2	64 ± 3	3.6 ± 0.2	3.2 ± 0.2	2.3 ± 0.2
6	25 ± 1	88 ± 3	3.7 ± 0.1	2.9 ± 0.2	2.5 ± 0.1
7	24 ± 2	93 ± 7	4.2 ± 0.1	4.0 ± 0.2	3.3 ± 0.2
8	26 ± 1	116 ± 8	4.6 ± 0.1	4.4 ± 0.2	3.8 ± 0.3

[a]0 = none of the isozyme loci has *G. soja* alleles; 1 = homozygous for the *Aco2-a* allele; 2 = homozygous for the *Aco4-b* allele; 3 = homozygous for the *Idh1-b* allele; 4 = homozygous for the *Dia1-b* allele; 5 = homozygous for the *Ap-a* allele; 6 = homozygous for the *Pgm1-a* allele; 7 = homozygous for the *Pgm2-b* allele; 8 = PI 342618A zymogram type for MDH.

Trait				
Burkey				
MAT	HT	LDG	PLT	VNG
19 ± 1	97 ± 3	3.7 ± 0.1	3.7 ± 0.1	2.8 ± 0.1
28 ± 2	133 ± 5	4.6 ± 0.1	4.3 ± 0.2	3.9 ± 0.2
23 ± 1	103 ± 3	4.1 ± 0.1	4.1 ± 0.1	3.3 ± 0.1
26 ± 2	112 ± 5	4.4 ± 0.2	4.4 ± 0.2	3.8 ± 0.2
13 ± 1	86 ± 4	3.8 ± 0.1	4.0 ± 0.1	2.7 ± 0.1
12 ± 1	70 ± 5	3.6 ± 0.2	4.1 ± 0.2	2.6 ± 0.2
21 ± 1	101 ± 3	3.9 ± 0.1	3.9 ± 0.1	2.9 ± 0.1
18 ± 2	96 ± 7	4.5 ± 0.1	4.5 ± 0.2	3.4 ± 0.2
22 ± 1	120 ± 7	4.4 ± 0.2	4.0 ± 0.4	3.8 ± 0.4

Table 19. Means and standard errors for each enzyme genotype in the 2-locus class for Cross 2 at individual locations

Enzyme locus genotype[a]	Trait				
	Ames				
	MAT	HT	LDG	PLT	VNG
0	24 ± 1	86 ± 3	3.5 ± 0.1	2.8 ± 0.1	2.4 ± 0.1
12	35 ± 3	113 ± 6	4.2 ± 0.2	4.2 ± 0.2	4.0 ± 0.2
13	31 ± 2	125 ± 7	4.7 ± 0.1	4.8 ± 0.1	4.6 ± 0.1
14	23 ± 2	103 ± 6	4.4 ± 0.1	4.2 ± 0.2	3.8 ± 0.2
15	16 ± 3	59 ± 6	3.5 ± 0.3	2.0 ± 0.4	1.5 ± 0.3
16	34 ± 2	133 ± 10	4.8 ± 0.1	4.8 ± 0.1	4.0 ± 0.4
17	28 ± 2	118 ± 6	4.8 ± 0.1	4.7 ± 0.2	4.5 ± 0.2
23	32 ± 2	139 ± 12	4.7 ± 0.2	4.5 ± 0.3	4.3 ± 0.3
24	21 ± 1	90 ± 4	3.9 ± 0.1	3.4 ± 0.2	2.8 ± 0.1
25	26 ± 2	79 ± 3	3.6 ± 0.1	3.1 ± 0.1	2.8 ± 0.1
26	26 ± 1	93 ± 4	3.6 ± 0.1	3.1 ± 0.2	2.7 ± 0.1
27	19 ± 2	71 ± 2	3.9 ± 0.2	3.0 ± 0.3	2.7 ± 0.3
28	22 ± 2	84 ± 5	4.2 ± 0.1	3.8 ± 0.3	3.2 ± 0.2
34	23 ± 1	101 ± 4	4.8 ± 0.1	4.3 ± 0.3	3.8 ± 0.3
36	35 ± 2	128 ± 5	4.5 ± 0.1	4.7 ± 0.1	4.2 ± 0.2
37	23 ± 4	112 ± 7	4.8 ± 0.1	4.7 ± 0.2	4.0 ± 0.3
45	13 ± 1	58 ± 2	3.5 ± 0.2	2.9 ± 0.2	2.4 ± 0.1
46	18 ± 1	84 ± 4	3.9 ± 0.1	3.4 ± 0.2	2.7 ± 0.1
47	16 ± 2	80 ± 7	4.2 ± 0.2	3.4 ± 0.3	2.8 ± 0.3
56	15 ± 2	57 ± 3	3.3 ± 0.3	2.6 ± 0.3	2.1 ± 0.2
57	13 ± 2	68 ± 4	3.8 ± 0.1	3.1 ± 0.3	2.6 ± 0.2
67	42 ± 2	111 ± 6	4.6 ± 0.1	4.8 ± 0.1	4.7 ± 0.2

[a]Each digit in the enzyme genotype indicates a locus that is homozygous for G. soja alleles. Refer to Table 18 for enzyme locus genotypes.

Trait				
Burkey				
MAT	HT	LDG	PLT	VNG
19 ± 1	97 ± 3	3.7 ± 0.1	3.7 ± 0.1	2.8 ± 0.1
28 ± 2	127 ± 5	4.4 ± 0.2	4.5 ± 0.3	3.6 ± 0.2
26 ± 2	130 ± 6	4.8 ± 0.1	4.8 ± 0.1	4.4 ± 0.2
20 ± 2	115 ± 5	4.5 ± 0.1	4.1 ± 0.2	3.7 ± 0.3
15 ± 2	62 ± 6	3.2 ± 0.5	2.8 ± 0.3	1.5 ± 0.5
29 ± 3	139 ± 6	4.6 ± 0.2	4.3 ± 0.3	4.0 ± 0.3
21 ± 1	136 ± 4	4.5 ± 0.2	4.2 ± 0.2	3.8 ± 0.2
29 ± 2	152 ± 7	4.7 ± 0.2	4.0 ± 0.6	4.2 ± 0.5
17 ± 1	97 ± 4	4.0 ± 0.1	4.1 ± 0.1	3.1 ± 0.1
22 ± 2	92 ± 4	4.0 ± 0.1	4.0 ± 0.2	2.8 ± 0.2
23 ± 1	104 ± 4	3.9 ± 0.1	4.1 ± 0.1	3.0 ± 0.1
16 ± 1	81 ± 4	4.4 ± 0.2	4.0 ± 0.5	2.7 ± 0.4
18 ± 1	96 ± 6	4.2 ± 0.1	3.9 ± 0.2	3.2 ± 0.2
18 ± 1	100 ± 5	4.4 ± 0.2	4.2 ± 0.3	3.8 ± 0.4
30 ± 2	132 ± 7	4.4 ± 0.1	4.1 ± 0.2	3.8 ± 0.2
19 ± 3	105 ± 4	4.6 ± 0.2	4.4 ± 0.3	4.2 ± 0.3
10 ± 1	67 ± 2	3.8 ± 0.2	4.1 ± 0.2	2.5 ± 0.2
13 ± 1	93 ± 4	3.7 ± 0.1	3.7 ± 0.2	2.6 ± 0.2
12 ± 1	82 ± 7	4.3 ± 0.2	4.5 ± 0.2	3.0 ± 0.3
13 ± 2	70 ± 5	3.8 ± 0.3	4.2 ± 0.2	2.9 ± 0.2
9 ± 2	75 ± 5	4.2 ± 0.3	3.9 ± 0.4	2.4 ± 0.2
34 ± 2	131 ± 7	4.6 ± 0.1	4.3 ± 0.3	4.0 ± 0.1

Table 20. Means and standard errors for each enzyme genotype in the 3-locus class for Cross 2 at individual locations

Enzyme locus genotype[a]	Trait				
	Ames				
	MAT	HT	LDG	PLT	VNG
0	24 ± 1	86 ± 3	3.5 ± 0.1	2.8 ± 0.1	2.4 ± 0.1
124	30 ± 1	102 ± 3	4.3 ± 0.2	3.3 ± 0.4	2.9 ± 0.3
125	28 ± 3	100 ± 6	4.1 ± 0.2	3.4 ± 0.3	2.8 ± 0.3
126	35 ± 3	123 ± 11	4.4 ± 0.1	3.7 ± 0.3	3.6 ± 0.3
134	24 ± 1	111 ± 10	4.7 ± 0.1	4.6 ± 0.2	4.0 ± 0.2
136	34 ± 2	119 ± 7	4.4 ± 0.1	4.3 ± 0.2	4.1 ± 0.2
137	37 ± 3	156 ± 5	4.5 ± 0.1	5.0 ± 0.0	4.8 ± 0.2
147	17 ± 1	97 ± 8	4.6 ± 0.1	3.9 ± 0.3	3.1 ± 0.3
167	29 ± 3	133 ± 8	4.8 ± 0.1	4.7 ± 0.2	4.5 ± 0.3
234	27 ± 2	99 ± 11	4.3 ± 0.2	3.8 ± 0.4	3.5 ± 0.3
236	39 ± 1	145 ± 14	4.4 ± 0.1	4.8 ± 0.2	4.7 ± 0.2
245	17 ± 2	68 ± 3	3.8 ± 0.2	3.3 ± 0.1	2.6 ± 0.2
246	25 ± 1	98 ± 4	3.7 ± 0.1	3.3 ± 0.2	3.0 ± 0.2
247	14 ± 2	67 ± 2	3.8 ± 0.2	3.0 ± 0.3	2.4 ± 0.2
248	24 ± 2	85 ± 7	3.9 ± 0.2	3.4 ± 0.3	3.1 ± 0.3
256	42 ± 2	120 ± 5	4.2 ± 0.1	4.1 ± 0.2	3.6 ± 0.2
257	16 ± 3	66 ± 3	3.6 ± 0.2	3.1 ± 0.3	2.3 ± 0.3
258	28 ± 4	79 ± 5	3.7 ± 0.3	3.1 ± 0.4	2.8 ± 0.3
268	34 ± 2	97 ± 5	4.2 ± 0.2	3.7 ± 0.3	3.2 ± 0.2
346	31 ± 2	124 ± 6	4.6 ± 0.1	4.6 ± 0.2	4.4 ± 0.2
347	25 ± 2	123 ± 5	4.5 ± 0.1	3.9 ± 0.3	3.5 ± 0.2
367	33 ± 3	118 ± 6	4.6 ± 0.1	4.5 ± 0.2	4.2 ± 0.3
456	8 ± 2	60 ± 2	3.6 ± 0.2	2.8 ± 0.4	2.1 ± 0.2
457	12 ± 2	65 ± 3	3.5 ± 0.2	2.9 ± 0.2	2.3 ± 0.2
467	26 ± 1	121 ± 7	4.5 ± 0.1	4.2 ± 0.2	3.9 ± 0.3

[a]Each digit in the enzyme genotype indicates a locus that is homozygous for *G. soja* alleles. Refer to Table 18 for enzyme locus genotypes.

Trait				
Burkey				
MAT	HT	LDG	PLT	VNG
19 ± 1	97 ± 3	3.7 ± 0.1	3.7 ± 0.1	2.8 ± 0.1
29 ± 2	105 ± 3	4.1 ± 0.2	3.6 ± 0.2	3.2 ± 0.4
22 ± 3	105 ± 9	4.1 ± 0.2	4.1 ± 0.3	3.1 ± 0.2
30 ± 3	134 ± 10	4.2 ± 0.2	3.9 ± 0.3	3.4 ± 0.3
19 ± 2	113 ± 7	4.7 ± 0.2	4.2 ± 0.3	4.1 ± 0.4
28 ± 2	137 ± 5	4.5 ± 0.1	4.5 ± 0.2	4.0 ± 0.2
30 ± 2	142 ± 7	4.4 ± 0.2	4.4 ± 0.3	4.4 ± 0.3
14 ± 1	100 ± 6	4.5 ± 0.2	4.1 ± 0.3	3.1 ± 0.3
24 ± 2	132 ± 6	4.7 ± 0.1	4.4 ± 0.3	4.6 ± 0.2
24 ± 2	111 ± 8	4.1 ± 0.2	3.4 ± 0.3	2.8 ± 0.3
39 ± 2	153 ± 7	4.6 ± 0.3	4.3 ± 0.4	4.2 ± 0.3
14 ± 2	81 ± 4	3.9 ± 0.1	3.6 ± 0.2	2.5 ± 0.2
22 ± 1	107 ± 5	3.9 ± 0.1	4.0 ± 0.1	3.3 ± 0.2
11 ± 1	73 ± 2	3.8 ± 0.2	3.6 ± 0.3	2.2 ± 0.3
19 ± 2	85 ± 6	4.1 ± 0.2	4.4 ± 0.3	3.1 ± 0.2
38 ± 2	131 ± 9	4.2 ± 0.2	4.2 ± 0.3	3.6 ± 0.3
13 ± 2	70 ± 4	3.7 ± 0.2	3.7 ± 0.3	2.3 ± 0.3
23 ± 4	93 ± 8	3.6 ± 0.2	4.0 ± 0.3	3.0 ± 0.3
32 ± 3	100 ± 6	4.3 ± 0.2	4.0 ± 0.2	3.2 ± 0.2
26 ± 2	135 ± 5	4.4 ± 0.1	4.3 ± 0.2	4.2 ± 0.2
19 ± 2	119 ± 7	4.4 ± 0.2	4.6 ± 0.2	3.7 ± 0.3
26 ± 2	132 ± 5	4.6 ± 0.1	4.4 ± 0.3	3.9 ± 0.2
7 ± 1	64 ± 3	3.4 ± 0.3	4.0 ± 0.3	2.1 ± 0.3
10 ± 1	72 ± 4	4.0 ± 0.2	3.4 ± 0.3	2.3 ± 0.2
21 ± 1	122 ± 7	4.4 ± 0.2	4.1 ± 0.3	3.5 ± 0.3

Table 21. Means and standard errors for each enzyme genotype in the 4-locus class for Cross 2 at individual locations

Enzyme locus genotype[a]	Trait				
	Ames				
	MAT	HT	LDG	PLT	VNG
0	24 ± 1	86 ± 3	3.5 ± 0.1	2.8 ± 0.1	2.4 ± 0.1
1245	17 ± 2	71 ± 4	4.3 ± 0.1	3.5 ± 0.3	2.7 ± 0.3
1246	34 ± 2	115 ± 8	4.1 ± 0.2	4.0 ± 0.5	3.8 ± 0.5
1367	29 ± 2	116 ± 7	4.8 ± 0.1	4.9 ± 0.1	4.7 ± 0.2
1467	18 ± 1	101 ± 5	4.5 ± 0.1	3.5 ± 0.3	3.4 ± 0.3
2368	18 ± 1	85 ± 2	4.0 ± 0.2	3.2 ± 0.4	2.4 ± 0.2
2456	25 ± 3	87 ± 7	3.8 ± 0.3	3.8 ± 0.4	3.2 ± 0.3
2457	10 ± 2	62 ± 4	4.5 ± 0.2	3.6 ± 0.5	2.5 ± 0.3
2458	27 ± 2	87 ± 10	4.2 ± 0.3	4.1 ± 0.3	3.6 ± 0.3
2468	23 ± 2	88 ± 4	4.5 ± 0.1	4.2 ± 0.3	3.5 ± 0.2
2568	41 ± 2	109 ± 6	4.2 ± 0.1	4.2 ± 0.2	4.0 ± 0.3
3467	22 ± 1	101 ± 8	4.8 ± 0.1	4.0 ± 0.3	3.3 ± 0.2

[a]Each digit in the enzyme genotype indicates a locus that is homozygous for G. soja alleles. Refer to Table 18 for enzyme locus genotypes.

Trait				
Burkey				
MAT	HT	LDG	PLT	VNG
19 ± 1	97 ± 3	3.7 ± 0.1	3.7 ± 0.1	2.8 ± 0.1
13 ± 2	85 ± 11	4.2 ± 0.2	4.3 ± 0.3	2.6 ± 0.3
29 ± 3	122 ± 6	4.4 ± 0.2	4.3 ± 0.4	3.3 ± 0.3
26 ± 1	123 ± 7	4.7 ± 0.1	4.1 ± 0.4	3.7 ± 0.3
12 ± 1	105 ± 6	4.5 ± 0.1	3.9 ± 0.3	3.3 ± 0.3
15 ± 1	89 ± 3	4.0 ± 0.2	3.5 ± 0.3	2.3 ± 0.2
22 ± 3	96 ± 9	4.0 ± 0.2	4.1 ± 0.3	3.1 ± 0.3
8 ± 1	67 ± 5	3.7 ± 0.2	3.5 ± 0.3	2.1 ± 0.3
23 ± 2	99 ± 9	4.0 ± 0.3	4.3 ± 0.3	3.6 ± 0.4
21 ± 3	89 ± 4	4.0 ± 0.2	3.3 ± 0.2	2.8 ± 0.2
36 ± 1	123 ± 11	4.1 ± 0.2	4.0 ± 0.4	3.6 ± 0.2
16 ± 1	106 ± 6	4.8 ± 0.1	4.4 ± 0.3	3.9 ± 0.3

Table 22. Means and standard errors for each enzyme genotype in the 5-locus class for Cross 2 at individual locations

Enzyme locus genotype[a]	Trait				
	Ames				
	MAT	HT	LDG	PLT	VNG
0	24 ± 1	86 ± 3	3.5 ± 0.1	2.8 ± 0.1	2.4 ± 0.1
12346	38 ± 3	142 ± 8	4.8 ± 0.1	4.9 ± 0.1	4.7 ± 0.2
13467	21 ± 2	114 ± 4	4.6 ± 0.1	4.2 ± 0.2	3.6 ± 0.3
23468	23 ± 1	87 ± 5	3.8 ± 0.2	2.0 ± 0.3	1.8 ± 0.1
24568	31 ± 2	93 ± 8	4.7 ± 0.2	4.7 ± 0.2	4.5 ± 0.2

[a]Each digit in the enzyme genotype indicates a locus that is homozygous for G. soja alleles. Refer to Table 18 for enzyme locus genotypes.

Trait				
Burkey				
MAT	HT	LDG	PLT	VNG
19 ± 1	97 ± 3	3.7 ± 0.1	3.7 ± 0.1	2.8 ± 0.1
31 ± 2	149 ± 5	4.4 ± 0.1	3.9 ± 0.3	4.2 ± 0.2
16 ± 2	116 ± 10	4.6 ± 0.1	4.3 ± 0.3	3.8 ± 0.2
17 ± 1	93 ± 2	3.5 ± 0.2	3.1 ± 0.3	2.2 ± 0.2
27 ± 2	111 ± 8	4.5 ± 0.1	4.5 ± 0.3	3.7 ± 0.2

Table 23. Means and standard errors for each enzyme genotype in the 1-locus class for Cross 1 averaged over two locations

Enzyme locus genotype[a]	Trait				
	MAT	HT	LDG	PLT	VNG
0	28 ± 1	102 ± 2	4.4 ± 0.0	4.0 ± 0.1	3.4 ± 0.1
1	23 ± 1	122 ± 5	4.2 ± 0.1	3.3 ± 0.2	3.1 ± 0.2
2	25 ± 1	92 ± 3	4.4 ± 0.1	4.1 ± 0.1	3.5 ± 0.1
3	28 ± 1	106 ± 3	4.6 ± 0.1	4.2 ± 0.1	3.5 ± 0.1
4	37 ± 1	116 ± 3	4.6 ± 0.0	4.5 ± 0.1	3.9 ± 0.1
5	29 ± 1	105 ± 3	4.5 ± 0.1	4.0 ± 0.1	3.4 ± 0.1
6	24 ± 1	103 ± 2	4.6 ± 0.0	4.0 ± 0.1	3.5 ± 0.1
PI 326581	21 ± 0	133 ± 5	5.0 ± 0.0	5.0 ± 0.0	5.0 ± 0.0
A80-244036	27 ± 0	90 ± 1	3.6 ± 0.1	2.5 ± 0.2	2.0 ± 0.1

[a]See Table 14 for enzyme locus genotypes.

Table 24. Means and standard errors for each enzyme genotype in the 2-locus class for Cross 1 averaged over two locations

Enzyme locus genotype[a]	Trait				
	MAT	HT	LDG	PLT	VNG
0	28 ± 1	102 ± 2	4.4 ± 0.0	4.0 ± 0.1	3.4 ± 0.1
12	24 ± 1	106 ± 5	4.7 ± 0.1	4.7 ± 0.1	4.1 ± 0.1
13	29 ± 1	120 ± 4	4.5 ± 0.1	4.3 ± 0.1	3.7 ± 0.1
14	43 ± 1	151 ± 5	4.8 ± 0.1	4.9 ± 0.1	4.6 ± 0.2
15	30 ± 1	134 ± 10	4.8 ± 0.1	5.0 ± 0.0	4.6 ± 0.2
16	20 ± 2	104 ± 4	4.6 ± 0.1	4.0 ± 0.2	3.4 ± 0.2
23	25 ± 1	94 ± 7	4.5 ± 0.1	4.4 ± 0.2	3.9 ± 0.2
24	28 ± 1	105 ± 5	4.4 ± 0.1	3.8 ± 0.2	3.3 ± 0.2
25	29 ± 0	116 ± 3	4.7 ± 0.1	4.3 ± 0.2	3.8 ± 0.2
26	24 ± 1	90 ± 3	4.7 ± 0.1	4.3 ± 0.1	3.5 ± 0.1
35	20 ± 1	88 ± 3	4.6 ± 0.1	3.7 ± 0.3	3.2 ± 0.3
36	21 ± 1	97 ± 6	4.7 ± 0.1	4.1 ± 0.2	3.5 ± 0.2
45	41 ± 1	130 ± 3	4.7 ± 0.0	4.6 ± 0.1	3.9 ± 0.1
46	38 ± 1	124 ± 4	4.9 ± 0.0	4.9 ± 0.1	4.5 ± 0.1
56	25 ± 1	107 ± 3	4.7 ± 0.1	4.3 ± 0.1	3.8 ± 0.1
PI 326581	21 ± 0	133 ± 5	5.0 ± 0.0	5.0 ± 0.0	5.0 ± 0.0
A80-244036	27 ± 0	90 ± 1	3.6 ± 0.1	2.5 ± 0.2	2.0 ± 0.1

[a]Each digit in the enzyme genotype indicates a locus that is homozygous for *G. soja* alleles. Refer to Table 14 for enzyme locus genotypes.

Table 25. Means and standard errors for each enzyme genotype in the 3-locus class for Cross 1 averaged over two locations

Enzyme locus genotype[a]	Trait				
	MAT	HT	LDG	PLT	VNG
0	28 ± 1	102 ± 2	4.4 ± 0.0	4.0 ± 0.1	3.4 ± 0.1
126	25 ± 1	96 ± 3	4.8 ± 0.1	4.6 ± 0.1	4.3 ± 0.2
134	40 ± 1	133 ± 4	4.7 ± 0.1	4.6 ± 0.1	4.1 ± 0.1
135	28 ± 1	129 ± 5	4.6 ± 0.1	4.5 ± 0.2	4.2 ± 0.2
136	30 ± 1	121 ± 4	4.8 ± 0.0	4.4 ± 0.1	4.0 ± 0.2
146	38 ± 1	126 ± 4	4.7 ± 0.1	4.8 ± 0.1	4.2 ± 0.1
156	20 ± 1	93 ± 4	4.7 ± 0.1	4.3 ± 0.2	3.8 ± 0.2
PI 326581	21 ± 0	133 ± 5	5.0 ± 0.0	5.0 ± 0.0	5.0 ± 0.0
A80-244036	27 ± 0	90 ± 1	3.6 ± 0.1	2.5 ± 0.2	2.0 ± 0.1

[a]Each digit in the enzyme genotype indicates a locus that is homozygous for G. soja alleles. Refer to Table 14 for enzyme locus genotypes.

Table 26. Means and standard errors for each enzyme genotype in the 4-locus class for Cross 1 averaged over two locations

Enzyme locus genotype[a]	Trait				
	MAT	HT	LDG	PLT	VNG
0	28 ± 1	102 ± 2	4.4 ± 0.0	4.0 ± 0.1	3.4 ± 0.1
1345	37 ± 1	137 ± 4	4.7 ± 0.1	4.9 ± 0.1	4.5 ± 0.1
1346	37 ± 1	146 ± 5	4.8 ± 0.1	4.5 ± 0.2	4.2 ± 0.2
1356	27 ± 1	115 ± 8	4.8 ± 0.1	4.4 ± 0.3	4.0 ± 0.3
PI 326581	21 ± 0	133 ± 5	5.0 ± 0.0	5.0 ± 0.0	5.0 ± 0.0
A80-244036	27 ± 0	90 ± 1	3.6 ± 0.1	2.5 ± 0.2	2.0 ± 0.1

[a]Each digit in the enzyme genotype indicates a locus that is homozygous for *G. soja* alleles. Refer to Table 14 for enzyme locus genotypes.

Table 27. Means and standard errors for each enzyme genotype in the 5-locus class for Cross 1 averaged over two locations

Enzyme locus genotype[a]	Trait				
	MAT	HT	LDG	PLT	VNG
0	28 ± 1	102 ± 2	4.4 ± 0.0	4.0 ± 0.1	3.4 ± 0.1
13456	32 ± 1	138 ± 6	4.7 ± 0.1	4.8 ± 0.1	4.5 ± 0.2
PI 326581	21 ± 0	133 ± 5	5.0 ± 0.0	5.0 ± 0.0	5.0 ± 0.0
A80-244036	27 ± 0	90 ± 1	3.6 ± 0.1	2.5 ± 0.2	2.0 ± 0.1

[a]Each digit in the enzyme genotype indicates a locus that is homozygous for G. soja alleles. Refer to Table 14 for enzyme locus genotypes.

Table 28. Means and standard errors for each enzyme genotype in the 1-locus class for Cross 2 averaged over two locations

Enzyme locus genotype[a]	Trait				
	MAT	HT	LDG	PLT	VNG
0	21 ± 1	92 ± 2	3.6 ± 0.1	3.2 ± 0.1	2.6 ± 0.1
1	30 ± 1	125 ± 4	4.6 ± 0.1	4.3 ± 0.2	4.0 ± 0.2
2	25 ± 1	98 ± 2	3.9 ± 0.1	3.6 ± 0.1	3.1 ± 0.1
3	29 ± 1	113 ± 3	4.4 ± 0.1	4.3 ± 0.2	3.7 ± 0.1
4	14 ± 1	82 ± 2	3.8 ± 0.1	3.5 ± 0.1	2.5 ± 0.1
5	13 ± 1	67 ± 3	3.6 ± 0.1	3.6 ± 0.2	2.4 ± 0.1
6	23 ± 1	95 ± 2	3.8 ± 0.1	3.4 ± 0.1	2.7 ± 0.1
7	21 ± 1	94 ± 5	4.4 ± 0.1	4.2 ± 0.2	3.3 ± 0.2
8	24 ± 1	118 ± 5	4.5 ± 0.1	4.2 ± 0.2	3.8 ± 0.2
PI 342618A	25 ± 0	141 ± 2	5.0 ± 0.0	5.0 ± 0.0	5.0 ± 0.0
A81-157007	24 ± 0	85 ± 1	2.5 ± 0.1	1.8 ± 0.1	1.5 ± 0.1

[a]See Table 18 for enzyme locus genotypes.

Table 29. Means and standard errors for each enzyme genotype in the 2-locus class for Cross 2 averaged over two locations

Enzyme locus genotype[a]	Trait				
	MAT	HT	LDG	PLT	VNG
0	21 ± 1	92 ± 2	3.6 ± 0.1	3.2 ± 0.1	2.6 ± 0.1
12	31 ± 2	120 ± 4	4.3 ± 0.1	4.4 ± 0.2	3.8 ± 0.2
13	29 ± 1	128 ± 4	4.8 ± 0.1	4.8 ± 0.1	4.5 ± 0.1
14	22 ± 1	109 ± 4	4.5 ± 0.1	4.1 ± 0.2	3.8 ± 0.2
15	15 ± 2	60 ± 4	3.4 ± 0.3	2.4 ± 0.3	1.5 ± 0.3
16	31 ± 2	136 ± 6	4.7 ± 0.1	4.6 ± 0.2	4.0 ± 0.2
17	25 ± 1	127 ± 4	4.6 ± 0.1	4.5 ± 0.2	4.2 ± 0.2
23	31 ± 1	145 ± 7	4.7 ± 0.1	4.3 ± 0.3	4.3 ± 0.3
24	19 ± 1	93 ± 3	3.9 ± 0.1	3.7 ± 0.1	3.0 ± 0.1
25	24 ± 1	86 ± 3	3.8 ± 0.1	3.6 ± 0.1	2.8 ± 0.1
26	24 ± 1	98 ± 3	3.7 ± 0.1	3.6 ± 0.1	2.9 ± 0.1
27	17 ± 1	76 ± 3	4.1 ± 0.1	3.5 ± 0.3	2.7 ± 0.2
28	20 ± 1	90 ± 4	4.2 ± 0.1	3.8 ± 0.2	3.2 ± 0.1
34	20 ± 1	101 ± 3	4.6 ± 0.1	4.2 ± 0.2	3.8 ± 0.2
36	33 ± 1	130 ± 4	4.4 ± 0.1	4.4 ± 0.1	4.0 ± 0.1
37	21 ± 2	108 ± 4	4.7 ± 0.1	4.6 ± 0.2	4.1 ± 0.2
45	11 ± 1	63 ± 2	3.6 ± 0.1	3.5 ± 0.2	2.4 ± 0.1
46	16 ± 1	88 ± 3	3.8 ± 0.1	3.5 ± 0.1	2.6 ± 0.1
47	14 ± 1	81 ± 5	4.2 ± 0.1	4.0 ± 0.2	2.9 ± 0.2
56	14 ± 1	63 ± 3	3.5 ± 0.2	3.4 ± 0.3	2.5 ± 0.2
57	11 ± 2	71 ± 3	4.0 ± 0.2	3.5 ± 0.3	2.5 ± 0.1
67	38 ± 2	121 ± 5	4.6 ± 0.1	4.6 ± 0.2	4.4 ± 0.1
PI 342618A	25 ± 0	141 ± 2	5.0 ± 0.0	5.0 ± 0.0	5.0 ± 0.0
A81-157007	24 ± 0	85 ± 1	2.5 ± 0.1	1.8 ± 0.1	1.5 ± 0.1

[a]Each digit in the enzyme genotype indicates a locus that is homozygous for G. soja alleles. Refer to Table 18 for enzyme locus genotypes.

Table 30. Means and standard errors for each enzyme genotype in the 3-locus class for Cross 2 averaged over two locations

Enzyme locus genotype[a]	Trait				
	MAT	HT	LDG	PLT	VNG
0	21 ± 1	92 ± 2	3.6 ± 0.1	3.2 ± 0.1	2.6 ± 0.1
124	29 ± 1	103 ± 2	4.2 ± 0.1	3.5 ± 0.2	3.1 ± 0.2
125	25 ± 2	102 ± 5	4.1 ± 0.2	3.8 ± 0.2	3.0 ± 0.2
126	33 ± 2	128 ± 7	4.3 ± 0.1	3.8 ± 0.2	3.5 ± 0.2
134	22 ± 1	112 ± 6	4.7 ± 0.1	4.4 ± 0.2	4.1 ± 0.2
136	31 ± 1	128 ± 5	4.4 ± 0.1	4.4 ± 0.1	4.1 ± 0.1
137	34 ± 2	149 ± 5	4.5 ± 0.1	4.7 ± 0.2	4.6 ± 0.2
147	15 ± 1	99 ± 5	4.6 ± 0.1	4.0 ± 0.2	3.1 ± 0.2
167	27 ± 2	133 ± 5	4.8 ± 0.1	4.6 ± 0.2	4.6 ± 0.2
234	26 ± 1	105 ± 7	4.2 ± 0.1	3.6 ± 0.2	3.2 ± 0.2
236	39 ± 1	149 ± 8	4.5 ± 0.1	4.6 ± 0.2	4.4 ± 0.2
245	16 ± 1	74 ± 3	3.8 ± 0.1	3.5 ± 0.1	2.6 ± 0.1
246	24 ± 1	103 ± 3	3.8 ± 0.1	3.6 ± 0.1	3.1 ± 0.1
247	12 ± 1	70 ± 2	3.8 ± 0.2	3.3 ± 0.2	2.3 ± 0.2
248	21 ± 1	85 ± 4	4.0 ± 0.1	3.9 ± 0.2	3.1 ± 0.2
256	40 ± 1	126 ± 5	4.2 ± 0.1	4.2 ± 0.2	3.6 ± 0.2
257	15 ± 2	68 ± 3	3.6 ± 0.1	3.4 ± 0.2	2.3 ± 0.2
258	26 ± 3	86 ± 5	3.7 ± 0.2	3.6 ± 0.3	2.9 ± 0.2
268	33 ± 2	98 ± 4	4.2 ± 0.1	3.9 ± 0.2	3.2 ± 0.2
346	28 ± 1	129 ± 4	4.5 ± 0.1	4.4 ± 0.1	4.3 ± 0.1
347	22 ± 2	121 ± 4	4.4 ± 0.1	4.3 ± 0.2	3.6 ± 0.2
367	30 ± 2	125 ± 4	4.6 ± 0.1	4.5 ± 0.2	4.1 ± 0.2
456	8 ± 1	62 ± 2	3.5 ± 0.2	3.4 ± 0.3	2.1 ± 0.2
457	11 ± 1	69 ± 3	3.7 ± 0.2	3.2 ± 0.2	2.3 ± 0.1
467	24 ± 1	121 ± 5	4.5 ± 0.1	4.2 ± 0.2	3.7 ± 0.2
PI 342618A	25 ± 0	141 ± 2	5.0 ± 0.0	5.0 ± 0.0	5.0 ± 0.0
A81-157007	24 ± 0	85 ± 1	2.5 ± 0.1	1.8 ± 0.1	1.5 ± 0.1

[a]Each digit in the enzyme genotype indicates a locus that is homozygous for G. soja alleles. Refer to Table 18 for enzyme locus genotypes.

Table 31. Means and standard errors for each enzyme genotype in the 4-locus class for Cross 2 averaged over two locations

Enzyme locus genotype[a]	Trait				
	MAT	HT	LDG	PLT	VNG
0	21 ± 1	92 ± 2	3.6 ± 0.1	3.2 ± 0.1	2.6 ± 0.1
1245	15 ± 1	78 ± 6	4.2 ± 0.1	3.9 ± 0.2	2.7 ± 0.2
1246	31 ± 2	118 ± 5	4.2 ± 0.2	4.2 ± 0.3	3.6 ± 0.3
1367	27 ± 1	120 ± 5	4.7 ± 0.1	4.5 ± 0.2	4.2 ± 0.2
1467	15 ± 1	103 ± 4	4.5 ± 0.1	3.7 ± 0.2	3.3 ± 0.2
2368	17 ± 1	87 ± 2	4.0 ± 0.2	3.4 ± 0.2	2.4 ± 0.1
2456	23 ± 2	92 ± 6	3.9 ± 0.2	4.0 ± 0.2	3.2 ± 0.2
2457	9 ± 1	64 ± 3	4.1 ± 0.2	3.6 ± 0.3	2.3 ± 0.2
2458	25 ± 1	93 ± 7	4.1 ± 0.2	4.2 ± 0.2	3.6 ± 0.2
2468	22 ± 2	89 ± 3	4.3 ± 0.1	3.8 ± 0.2	3.2 ± 0.2
2568	39 ± 1	116 ± 6	4.1 ± 0.1	4.1 ± 0.2	3.8 ± 0.2
3467	19 ± 1	103 ± 5	4.8 ± 0.1	4.2 ± 0.2	3.6 ± 0.2
PI 342618A	25 ± 0	141 ± 2	5.0 ± 0.0	5.0 ± 0.0	5.0 ± 0.0
A81-157007	24 ± 0	85 ± 1	2.5 ± 0.1	1.8 ± 0.1	1.5 ± 0.1

[a]Each digit in the enzyme genotype indicates a locus that is homozygous for G. soja alleles. Refer to Table 18 for enzyme locus genotypes.

Table 32. Means and standard errors for each enzyme genotype in the 5-locus class for Cross 2 averaged over two locations

Enzyme locus genotype[a]	Trait				
	MAT	HT	LDG	PLT	VNG
0	21 ± 1	92 ± 2	3.6 ± 0.1	3.2 ± 0.1	2.6 ± 0.1
12346	35 ± 2	145 ± 5	4.6 ± 0.1	4.4 ± 0.2	4.5 ± 0.1
13467	18 ± 1	115 ± 5	4.6 ± 0.1	4.3 ± 0.2	3.7 ± 0.2
23468	20 ± 1	90 ± 3	3.6 ± 0.2	2.6 ± 0.2	2.0 ± 0.1
24568	29 ± 1	102 ± 6	4.6 ± 0.1	4.6 ± 0.2	4.1 ± 0.2
PI 342618A	25 ± 0	141 ± 2	5.0 ± 0.0	5.0 ± 0.0	5.0 ± 0.0
A81-157007	24 ± 0	85 ± 1	2.5 ± 0.1	1.8 ± 0.1	1.5 ± 0.1

[a]Each digit in the enzyme genotype indicates a locus that is homozygous for G. soja alleles. Refer to Table 18 for enzyme locus genotypes.

The enzyme genotypes that were associated with effects on quantitative traits in Cross 1 were different from the specific associations that were found in Cross 2. In Cross 1, lines that were homozygous for G. soja alleles at the Pgm1 locus were about 10 d later in maturity and had a greater plant height than random BC_2F_4-derived lines that had retained no G. soja alleles at any of the marker loci (Table 23). The Idh2 locus was associated with genes that affected MAT and HT. Lines that were homozygous for alleles from G. soja PI 326581 at the Ap, Pgm1, and Pgi loci were associated with poorer LDG scores. The Aco2 locus was associated with a better average plant type than the 0 class, while the Pgm1 locus was associated with poorer plant type and greater vining. For Cross 2, the Aco2, Aco4, and Idh1 loci were associated with later maturity, while lines that were homozygous for alleles from G. soja PI 342618A at the Dia1 and Ap loci matured earlier than the 0 class (Table 28). The Aco2, Idh1, and MDH loci were associated with an increase in HT. Glycine soja alleles at the Aco2, Aco4, Idh1, Pgm2, and MDH loci were associated with poorer LDG scores compared with random lines in the 0 class. All enzyme genotypes except Pgm1-a homozygotes were associated with an increase in PLT score, and lines homozygous for G. soja alleles at any of the marker loci except Dia1, Ap, and Pgm1 had increased vining (Table 28).

Each enzyme locus genotype was represented by as many families as possible. Differences among families within enzyme genotypes provided evidence that the effects observed for different enzyme locus genotypes were due to factors linked to the marker loci and not to pleiotropic action of the marker genes (Tables 33 through 77). For

Table 33. Means and standard errors for date of maturity for families within each enzyme locus genotype in the 1-locus class for Cross 1 averaged over two locations

Enzyme locus genotype[b]	Family[a]									
	1-2	12-2	15-1	16-6	21-1	6-1	6-3	7-1	8-3	8-4
0	21 ± 1	33 ± 2	23 ± 1	26 ± 1	25 ± 1	36 ± 2	29 ± 1	22 ± 1	29 ± 1	34 ± 1
1	—	—	—	—	—	—	—	23 ± 1	—	—
2	—	—	22 ± 1	26 ± 1	30 ± 1	—	—	—	—	—
3	22 ± 1	—	—	—	33 ± 2	—	—	—	—	29 ± 1
4	18 ± 1	42 ± 1	—	—	43 ± 1	37 ± 2	—	—	41 ± 2	32 ± 2
5	24 ± 1	31 ± 2	—	—	—	—	—	—	37 ± 3	—
6	18 ± 1	—	—	24 ± 1	24 ± 1	—	27 ± 2	21 ± 1	26 ± 1	32 ± 2

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 14 for enzyme genotypes.

Table 34. Means and standard errors for height for families within each enzyme locus genotype in the 1-locus class for Cross 1 averaged over two locations

Enzyme locus genotype[b]	Family[a] 1-2	12-2	15-1	16-6	21-1	6-1	6-3	7-1	8-3	8-4
0	91 ± 3	124 ± 4	85 ± 5	92 ± 4	104 ± 4	113 ± 5	103 ± 5	89 ± 4	103 ± 4	123 ± 5
1	—	—	—	—	—	—	—	122 ± 5	—	—
2	—	—	84 ± 3	88 ± 4	123 ± 9	—	—	—	—	—
3	94 ± 4	—	—	—	105 ± 5	—	—	—	—	120 ± 5
4	88 ± 3	130 ± 5	—	—	117 ± 6	118 ± 6	—	—	111 ± 7	115 ± 6
5	99 ± 3	115 ± 7	—	—	—	—	—	—	109 ± 8	—
6	87 ± 4	—	—	87 ± 6	112 ± 4	—	108 ± 4	104 ± 4	104 ± 4	121 ± 7

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 14 for enzyme genotypes.

Table 35. Means and standard errors for lodging for families within each enzyme locus genotype in the 1-locus class for Cross 1 averaged over two locations

Enzyme locus genotype[b]	Family[a]			
	1-2	12-2	15-1	16-6
0	4.5 ± 0.1	4.7 ± 0.1	3.9 ± 0.2	4.7 ± 0.1
1	—	—	—	—
2	—	—	4.1 ± 0.1	4.4 ± 0.1
3	4.5 ± 0.1	—	—	—
4	4.6 ± 0.2	4.5 ± 0.1	—	—
5	4.4 ± 0.1	4.6 ± 0.1	—	—
6	4.4 ± 0.1	—	—	4.8 ± 0.1

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 14 for enzyme genotypes.

Family[a]					
21-1	6-1	6-3	7-1	8-3	8-4
4.7 ± 0.1	4.4 ± 0.1	4.1 ± 0.1	4.0 ± 0.1	4.5 ± 0.1	4.7 ± 0.1
—	—	—	4.2 ± 0.1	—	—
4.7 ± 0.1	—	—	—	—	—
4.6 ± 0.1	—	—	—	—	4.7 ± 0.1
4.6 ± 0.1	4.5 ± 0.1	—	—	4.6 ± 0.1	4.8 ± 0.1
—	—	—	—	4.5 ± 0.2	—
4.7 ± 0.1	—	4.4 ± 0.1	4.3 ± 0.1	4.6 ± 0.1	4.8 ± 0.1

Table 36. Means and standard errors for plant type for families within each enzyme locus genotype in the 1-locus class for Cross 1 averaged over two locations

Enzyme locus genotype[b]	Family[a]			
	1-2	12-2	15-1	16-6
0	4.0 ± 0.2	4.4 ± 0.2	3.7 ± 0.2	4.4 ± 0.2
1	—	—	—	—
2	—	—	3.6 ± 0.2	4.3 ± 0.2
3	4.0 ± 0.2	—	—	—
4	4.5 ± 0.3	4.6 ± 0.2	—	—
5	3.8 ± 0.2	4.1 ± 0.2	—	—
6	3.9 ± 0.2	—	—	4.4 ± 0.2

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 14 for enzyme genotypes.

Family[a]					
21-1	6-1	6-3	7-1	8-3	8-4
4.4 ± 0.2	4.0 ± 0.2	3.4 ± 0.2	3.7 ± 0.2	3.8 ± 0.2	4.8 ± 0.1
—	—	—	3.4 ± 0.2	—	—
5.0 ± 0.0	—	—	—	—	—
4.3 ± 0.2	—	—	—	—	4.3 ± 0.2
4.7 ± 0.1	4.1 ± 0.2	—	—	4.4 ± 0.3	5.0 ± 0.0
—	—	—	—	4.3 ± 0.2	—
4.4 ± 0.2	—	3.9 ± 0.2	3.6 ± 0.2	3.8 ± 0.2	4.8 ± 0.2

Table 37. Means and standard errors for vining for families within each enzyme locus genotype in the 1-locus class for Cross 1 averaged over two locations

Enzyme locus genotype[b]	Family[a]			
	1-2	12-2	15-1	16-6
0	3.3 ± 0.2	3.9 ± 0.2	3.0 ± 0.2	3.9 ± 0.2
1	—	—	—	—
2	—	—	3.0 ± 0.2	3.7 ± 0.2
3	3.5 ± 0.2	—	—	—
4	3.8 ± 0.3	4.0 ± 0.2	—	—
5	3.2 ± 0.2	3.8 ± 0.3	—	—
6	3.4 ± 0.2	—	—	4.3 ± 0.3

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 14 for enzyme genotypes.

Family[a]					
21-1	6-1	6-3	7-1	8-3	8-4
3.8 ± 0.2	3.4 ± 0.2	2.8 ± 0.2	3.0 ± 0.2	3.1 ± 0.2	4.2 ± 0.2
—	—	—	3.1 ± 0.2	—	—
4.5 ± 0.2	—	—	—	—	—
3.4 ± 0.2	—	—	—	—	3.7 ± 0.2
4.0 ± 0.1	3.5 ± 0.2	—	—	3.8 ± 0.2	4.8 ± 0.1
—	—	—	—	3.5 ± 0.2	—
3.6 ± 0.2	—	3.3 ± 0.2	3.0 ± 0.2	3.2 ± 0.2	4.2 ± 0.2

Table 38. Means and standard errors for maturity for families within each enzyme locus genotype in the 2-locus class for Cross 1 averaged over two locations

Enzyme locus genotype[b]	Family[a] 1-2	12-2	15-1	16-6	21-1	6-1	6-3	7-1	8-3	8-4
0	21 ± 1	33 ± 2	23 ± 1	26 ± 1	25 ± 1	36 ± 2	29 ± 1	22 ± 1	29 ± 1	34 ± 1
12	—	—	—	24 ± 1	25 ± 2	—	—	—	—	—
13	—	—	—	—	23 ± 1	—	—	—	—	34 ± 2
14	—	—	—	—	43 ± 1	—	—	—	—	—
15	—	—	—	—	—	—	—	—	—	30 ± 1
16	—	—	—	—	26 ± 3	—	—	15 ± 2	—	—
23	—	—	—	25 ± 1	—	—	—		—	—
24	—	—	—	—	29 ± 2	—	—	—	28 ± 0	—
25	—	—	—	—	—	—	—	—	—	29 ± 0
26	—	—	—	26 ± 1	22 ± 1	—	—	—	—	—
35	20 ± 1	—	—	—	—	—	—	—	—	—
36	19 ± 1	—	—	—	23 ± 0	—	—	—	—	—
45	—	43 ± 1	—	—	—	—	—	—	36 ± 1	—
46	—	—	—	—	39 ± 1	—	—	—	—	37 ± 1
56	19 ± 0	—	—	—	—	38 ± 2	—	—	—	28 ± 2

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 14 for enzyme genotypes.

Table 39. Means and standard errors for height for families within each enzyme locus genotype in the 2-locus class for Cross 1 averaged over two locations

Enzyme locus genotype[b]	Family[a] 1-2	12-2	15-1	16-6	21-1	6-1	6-3	7-1	8-3	8-4
0	91 ± 3	124 ± 4	85 ± 5	92 ± 4	104 ± 4	113 ± 5	103 ± 5	89 ± 4	103 ± 4	123 ± 5
12	—	—	—	105 ± 6	107 ± 8	—	—	—	—	—
13	—	—	—	—	104 ± 6	—	—	—	—	132 ± 5
14	—	—	—	—	151 ± 5	—	—	—	—	—
15	—	—	—	—	—	—	—	—	—	134 ± 10
16	—	—	—	—	115 ± 5	—	—	94 ± 6	—	—
23	—	—	—	94 ± 7	—	—	—	—	—	—
24	—	—	—	—	102 ± 6	—	—	—	109 ± 8	—
25	—	—	—	—	—	—	—	—	—	116 ± 3
26	—	—	—	83 ± 3	98 ± 6	—	—	—	—	—
35	88 ± 3	—	—	—	—	—	—	—	—	—
36	88 ± 4	—	—	—	106 ± 9	—	—	—	—	—
45	—	132 ± 4	—	—	—	—	—	—	125 ± 3	—
46	—	—	—	—	117 ± 6	—	—	—	—	128 ± 5
56	94 ± 3	—	—	—	—	104 ± 1	—	—	—	118 ± 5

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 14 for enzyme genotypes.

Table 40. Means and standard errors for lodging for families within each enzyme locus genotype in the 2-locus class for Cross 1 averaged over two locations

Enzyme locus genotype[b]	Family[a]			
	1-2	12-2	15-1	16-6
0	4.5 ± 0.1	4.7 ± 0.1	3.9 ± 0.2	4.7 ± 0.1
12	—	—	—	4.7 ± 0.1
13	—	—	—	—
14	—	—	—	—
15	—	—	—	—
16	—	—	—	—
23	—	—	—	4.5 ± 0.1
24	—	—	—	—
25	—	—	—	—
26	—	—	—	4.6 ± 0.1
35	4.6 ± 0.1	—	—	—
36	4.6 ± 0.1	—	—	—
45	—	4.7 ± 0.1	—	—
46	—	—	—	—
56	4.8 ± 0.1	—	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 14 for enzyme genotypes.

Family[a]					
21-1	6-1	6-3	7-1	8-3	8-4
4.7 ± 0.1	4.4 ± 0.1	4.1 ± 0.1	4.0 ± 0.1	4.5 ± 0.1	4.7 ± 0.1
4.7 ± 0.1	—	—	—	—	—
4.3 ± 0.2	—	—	—	—	4.7 ± 0.0
4.8 ± 0.1	—	—	—	—	—
—	—	—	—	—	4.8 ± 0.1
4.6 ± 0.1	—	—	4.5 ± 0.1	—	—
—	—	—	—	—	—
4.2 ± 0.1	—	—	—	4.7 ± 0.1	—
—	—	—	—	—	4.7 ± 0.1
4.8 ± 0.1	—	—	—	—	—
—	—	—	—	—	—
4.8 ± 0.1	—	—	—	—	—
—	—	—	—	4.7 ± 0.1	—
5.0 ± 0.0	—	—	—	—	4.8 ± 0.1
—	4.3 ± 0.3	—	—	—	4.8 ± 0.1

Table 41. Means and standard errors for plant type for families within each enzyme locus genotype in the 2-locus class for Cross 1 averaged over two locations

Enzyme locus genotype[b]	Family[a]			
	1-2	12-2	15-1	16-6
0	4.0 ± 0.2	4.4 ± 0.2	3.7 ± 0.2	4.4 ± 0.2
12	—	—	—	4.8 ± 0.1
13	—	—	—	—
14	—	—	—	—
15	—	—	—	—
16	—	—	—	—
23	—	—	—	4.4 ± 0.2
24	—	—	—	—
25	—	—	—	—
26	—	—	—	4.3 ± 0.2
35	3.7 ± 0.3	—	—	—
36	3.8 ± 0.3	—	—	—
45	—	4.8 ± 0.1	—	—
46	—	—	—	—
56	4.3 ± 0.2	—	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 14 for enzyme genotypes.

Family[a]					
21-1	6-1	6-3	7-1	8-3	8-4
4.4 ± 0.2	4.0 ± 0.2	3.4 ± 0.2	3.7 ± 0.2	3.8 ± 0.2	4.8 ± 0.1
4.5 ± 0.2	—	—	—	—	—
4.1 ± 0.2	—	—	—	—	4.5 ± 0.2
4.9 ± 0.1	—	—	—	—	—
—	—	—	—	—	5.0 ± 0.0
4.4 ± 0.2	—	—	3.7 ± 0.2	—	—
—	—	—	—	—	—
3.5 ± 0.3	—	—	—	4.1 ± 0.3	—
—	—	—	—	—	4.3 ± 0.2
4.4 ± 0.2	—	—	—	—	—
—	—	—	—	—	—
4.8 ± 0.3	—	—	—	—	—
—	—	—	—	4.3 ± 0.2	—
5.0 ± 0.0	—	—	—	—	4.9 ± 0.1
—	4.8 ± 0.3	—	—	—	4.3 ± 0.2

Table 42. Means and standard errors for vining for families within each enzyme locus genotype in the 2-locus class for Cross 1 averaged over two locations

Enzyme locus genotype[b]	Family[a] 1-2	12-2	15-1	16-6
0	3.3 ± 0.2	3.9 ± 0.2	3.0 ± 0.2	3.9 ± 0.2
12	—	—	—	4.2 ± 0.2
13	—	—	—	—
14	—	—	—	—
15	—	—	—	—
16	—	—	—	—
23	—	—	—	3.9 ± 0.2
24	—	—	—	—
25	—	—	—	—
26	—	—	—	3.8 ± 0.2
35	3.2 ± 0.3	—	—	—
36	3.4 ± 0.4	—	—	—
45	—	4.1 ± 0.1	—	—
46	—	—	—	—
56	3.8 ± 0.2	—	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 14 for enzyme genotypes.

Family[a]					
21-1	6-1	6-3	7-1	8-3	8-4
3.8 ± 0.2	3.4 ± 0.2	2.8 ± 0.2	3.0 ± 0.2	3.1 ± 0.2	4.2 ± 0.2
4.1 ± 0.2	—	—	—	—	—
3.3 ± 0.2	—	—	—	—	4.1 ± 0.2
4.6 ± 0.2	—	—	—	—	—
—	—	—	—	—	4.6 ± 0.2
3.8 ± 0.3	—	—	3.1 ± 0.2	—	—
—	—	—	—	—	—
3.0 ± 0.2	—	—	—	3.8 ± 0.3	—
—	—	—	—	—	3.8 ± 0.2
3.1 ± 0.2	—	—	—	—	—
—	—	—	—	—	—
3.6 ± 0.3	—	—	—	—	—
—	—	—	—	3.6 ± 0.3	—
4.6 ± 0.2	—	—	—	—	4.5 ± 0.2
—	3.8 ± 0.3	—	—	—	3.7 ± 0.3

Table 43. Means and standard errors for maturity for families within each enzyme locus genotype in the 3-locus class for Cross 1 averaged over two locations

Enzyme locus genotype[b]	Family[a]									
	1-2	12-2	15-1	16-6	21-1	6-1	6-3	7-1	8-3	8-4
0	21 ± 1	33 ± 2	23 ± 1	26 ± 1	25 ± 1	36 ± 2	29 ± 1	22 ± 1	29 ± 1	34 ± 1
126	—	—	—	25 ± 1	—	—	—	—	—	—
134	—	—	—	—	41 ± 1	—	—	—	—	38 ± 2
135	—	—	—	—	—	—	—	—	—	28 ± 1
136	—	—	—	—	34 ± 3	—	—	—	—	27 ± 1
146	—	—	—	—	40 ± 1	—	—	—	—	36 ± 1
156	20 ± 1	—	—	—	—	—	—	—	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 14 for enzyme genotypes.

Table 44. Means and standard errors for height for families within each enzyme locus genotype in the 3-locus class for Cross 1 averaged over two locations

Enzyme locus genotype[b]	Family[a]									
	1-2	12-2	15-1	16-6	21-1	6-1	6-3	7-1	8-3	8-4
0	91 ± 3	124 ± 4	85 ± 5	92 ± 4	104 ± 4	113 ± 5	103 ± 5	89 ± 4	103 ± 4	123 ± 5
126	—	—	—	96 ± 3	—	—	—	—	—	—
134	—	—	—	—	131 ± 5	—	—	—	—	139 ± 6
135	—	—	—	—	—	—	—	—	—	129 ± 5
136	—	—	—	—	131 ± 8	—	—	—	—	115 ± 3
146	—	—	—	—	130 ± 7	—	—	—	—	121 ± 5
156	93 ± 4	—	—	—	—	—	—	—	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 14 for enzyme genotypes.

Table 45. Means and standard errors for lodging for families within each enzyme locus genotype in the 3-locus class for Cross 1 averaged over two locations

Enzyme locus genotype[b]	Family[a]			
	1-2	12-2	15-1	16-6
0	4.5 ± 0.1	4.7 ± 0.1	3.9 ± 0.2	4.7 ± 0.1
126	—	—	—	4.8 ± 0.1
134	—	—	—	—
135	—	—	—	—
136	—	—	—	—
146	—	—	—	—
156	4.7 ± 0.1	—	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 14 for enzyme genotypes.

Family[a]					
21-1	6-1	6-3	7-1	8-3	8-4
4.7 ± 0.1	4.4 ± 0.1	4.1 ± 0.1	4.0 ± 0.1	4.5 ± 0.1	4.7 ± 0.1
—	—	—	—	—	—
4.7 ± 0.1	—	—	—	—	4.7 ± 0.1
—	—	—	—	—	4.6 ± 0.1
4.8 ± 0.0	—	—	—	—	4.7 ± 0.1
4.7 ± 0.1	—	—	—	—	4.7 ± 0.1
—	—	—	—	—	—

Table 46. Means and standard errors for plant type for families within each enzyme locus genotype in the 3-locus class for Cross 1 averaged over two locations

Enzyme locus genotype[b]	Family[a]			
	1-2	12-2	15-1	16-6
0	4.0 ± 0.2	4.4 ± 0.2	3.7 ± 0.2	4.4 ± 0.2
126	—	—	—	4.6 ± 0.1
134	—	—	—	—
135	—	—	—	—
136	—	—	—	—
146	—	—	—	—
156	4.3 ± 0.2	—	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 14 for enzyme genotypes.

Family[a]					
21-1	6-1	6-3	7-1	8-3	8-4
4.4 ± 0.2	4.0 ± 0.2	3.4 ± 0.2	3.7 ± 0.2	3.8 ± 0.2	4.8 ± 0.1
—	—	—	—	—	—
4.6 ± 0.2	—	—	—	—	4.9 ± 0.1
—	—	—	—	—	4.5 ± 0.2
4.7 ± 0.2	—	—	—	—	4.3 ± 0.2
4.8 ± 0.1	—	—	—	—	4.8 ± 0.1
—	—	—	—	—	—

Table 47. Means and standard errors for vining for families within each enzyme locus genotype in the 3-locus class for Cross 1 averaged over two locations

Enzyme locus genotype[b]	Family[a]			
	1-2	12-2	15-1	16-6
0	3.3 ± 0.2	3.9 ± 0.2	3.0 ± 0.2	3.9 ± 0.2
126	—	—	—	4.3 ± 0.2
134	—	—	—	—
135	—	—	—	—
136	—	—	—	—
146	—	—	—	—
156	3.8 ± 0.2	—	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 14 for enzyme genotypes.

Family[a]					
21-1	6-1	6-3	7-1	8-3	8-4
3.8 ± 0.2	3.4 ± 0.2	2.8 ± 0.2	3.0 ± 0.2	3.1 ± 0.2	4.2 ± 0.2
—	—	—	—	—	—
4.0 ± 0.2	—	—	—	—	4.6 ± 0.2
—	—	—	—	—	4.2 ± 0.2
3.9 ± 0.2	—	—	—	—	4.1 ± 0.2
4.2 ± 0.2	—	—	—	—	4.3 ± 0.2
—	—	—	—	—	—

Table 48. Means and standard errors for maturity for families within each enzyme locus genotype in the 4- and 5-locus classes for Cross 1 averaged over two locations

Enzyme locus genotype[b]	Family[a]									
	1-2	12-2	15-1	16-6	21-1	6-1	6-3	7-1	8-3	8-4
0	21 ± 1	33 ± 2	23 ± 1	26 ± 1	25 ± 1	36 ± 2	29 ± 1	22 ± 1	29 ± 1	34 ± 1
1345	—	—	—	—	—	—	—	—	—	37 ± 1
1346	—	—	—	—	—	—	—	—	—	37 ± 1
1356	—	—	—	—	—	—	—	—	—	27 ± 1
13456	—	—	—	—	—	—	—	—	—	32 ± 1

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 14 for enzyme genotypes.

Table 49. Means and standard errors for height for families within each enzyme locus genotype in the 4-locus class for Cross 1 averaged over two locations

Enzyme locus genotype[b]	Family[a] 1-2	12-2	15-1	16-6	21-1	6-1	6-3	7-1	8-3	8-4
0	91 ± 3	124 ± 4	85 ± 5	92 ± 4	104 ± 4	113 ± 5	103 ± 5	89 ± 4	103 ± 4	123 ± 5
1345	—	—	—	—	—	—	—	—	—	138 ± 4
1346	—	—	—	—	—	—	—	—	—	146 ± 5
1356	—	—	—	—	—	—	—	—	—	115 ± 8
13456	—	—	—	—	—	—	—	—	—	138 ± 6

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 14 for enzyme genotypes.

Table 50. Means and standard errors for lodging for families within each enzyme locus genotype in the 4-locus class for Cross 1 averaged over two locations

Enzyme locus genotype[b]	Family[a]			
	1-2	12-2	15-1	16-6
0	4.5 ± 0.1	4.7 ± 0.1	3.9 ± 0.2	4.7 ± 0.1
1345	—	—	—	—
1346	—	—	—	—
1356	—	—	—	—
13456	—	—	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 14 for enzyme genotypes.

Family[a]					
21-1	6-1	6-3	7-1	8-3	8-4
4.7 ± 0.1	4.4 ± 0.1	4.1 ± 0.1	4.0 ± 0.1	4.5 ± 0.1	4.7 ± 0.1
—	—	—	—	—	4.7 ± 0.1
—	—	—	—	—	4.8 ± 0.1
—	—	—	—	—	4.8 ± 0.1
—	—	—	—	—	4.7 ± 0.1

Table 51. Means and standard errors for plant type for families within each enzyme locus genotype in the 4-locus class for Cross 1 averaged over two locations

Enzyme locus genotype[b]	Family[a]			
	1-2	12-2	15-1	16-6
0	4.0 ± 0.2	4.4 ± 0.2	3.7 ± 0.2	4.4 ± 0.2
1345	—	—	—	—
1346	—	—	—	—
1356	—	—	—	—
13456	—	—	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 14 for enzyme genotypes.

Family[a]					
21-1	6-1	6-3	7-1	8-3	8-4
4.4 ± 0.2	4.0 ± 0.2	3.4 ± 0.2	3.7 ± 0.2	3.8 ± 0.2	4.8 ± 0.1
—	—	—	—	—	4.9 ± 0.1
—	—	—	—	—	4.5 ± 0.2
—	—	—	—	—	4.4 ± 0.3
—	—	—	—	—	4.8 ± 0.1

Table 52. Means and standard errors for vining for families within each enzyme locus genotype in the 4-locus class for Cross 1 averaged over two locations

Enzyme locus genotype[b]	Family[a]			
	1-2	12-2	15-1	16-6
0	3.3 ± 0.2	3.9 ± 0.2	3.0 ± 0.2	3.9 ± 0.2
1345	—	—	—	—
1346	—	—	—	—
1356	—	—	—	—
13456	—	—	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 14 for enzyme genotypes.

Family[a]					
21-1	6-1	6-3	7-1	8-3	8-4
3.8 ± 0.2	3.4 ± 0.2	2.8 ± 0.2	3.0 ± 0.2	3.1 ± 0.2	4.2 ± 0.2
—	—	—	—	—	4.5 ± 0.1
—	—	—	—	—	4.2 ± 0.2
—	—	—	—	—	4.0 ± 0.3
—	—	—	—	—	4.5 ± 0.2

Table 53. Means and standard errors for date of maturity for families within each enzyme locus genotype in the 1-locus class for Cross 2 averaged over two locations

Enzyme locus genotype[b]	Family[a]									
	11-1	11-2	11-4	14-1	14-2	14-4	14-5	15-1	15-2	9-3
0	17 ± 1	18 ± 1	29 ± 1	15 ± 1	15 ± 1	—	—	26 ± 1	29 ± 3	27 ± 2
1	—	—	—	—	—	—	—	30 ± 2	31 ± 2	—
2	17 ± 1	18 ± 1	26 ± 1	—	17 ± 1	27 ± 2	31 ± 2	23 ± 1	32 ± 2	32 ± 1
3	—	—	—	—	—	—	—	31 ± 1	26 ± 3	—
4	13 ± 1	—	20 ± 2	11 ± 1	9 ± 0	—	—	16 ± 1	—	—
5	—	—	—	13 ± 2	13 ± 1	—	—	—	—	—
6	14 ± 1	18 ± 1	22 ± 1	20 ± 1	17 ± 1	—	—	23 ± 1	40 ± 2	25 ± 1
7	—	—	—	—	17 ± 1	—	—	25 ± 2	—	—
8	—	—	—	—	—	—	—	24 ± 1	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 18 for enzyme genotype.

Table 54. Means and standard errors for height for families within each enzyme locus genotype in the 1-locus class for Cross 2 averaged over two locations

Enzyme locus genotype[b]	Family[a]									
	11-1	11-2	11-4	14-1	14-2	14-4	14-5	15-1	15-2	9-3
0	77 ± 4	83 ± 3	119 ± 4	66 ± 2	73 ± 5	—	—	126 ± 6	105 ± 7	87 ± 2
1	—	—	—	—	—	—	—	122 ± 6	130 ± 6	—
2	76 ± 3	88 ± 3	106 ± 4	—	67 ± 2	91 ± 5	104 ± 4	130 ± 5	131 ± 4	90 ± 3
3	—	—	—	—	—	—	—	116 ± 3	110 ± 6	—
4	74 ± 3	—	101 ± 7	66 ± 2	66 ± 2	—	—	103 ± 4	—	—
5	—	—	—	59 ± 5	74 ± 3	—	—	—	—	—
6	84 ± 3	78 ± 2	107 ± 6	73 ± 3	70 ± 2	—	—	100 ± 5	134 ± 6	90 ± 2
7	—	—	—	—	70 ± 3	—	—	119 ± 4	—	—
8	—	—	—	—	—	—	—	118 ± 5	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 18 for enzyme genotypes.

Table 55. Means and standard errors for lodging for families within each enzyme locus genotype in the 1-locus class for Cross 2 averaged over two locations

Enzyme locus genotype[b]	Family[a]			
	11-1	11-2	11-4	14-1
0	3.7 ± 0.2	3.6 ± 0.2	3.8 ± 0.2	3.0 ± 0.2
1	—	—	—	—
2	3.0 ± 0.2	3.6 ± 0.1	3.7 ± 0.2	3.1 ± 0.2
3	—	—	—	—
4	4.0 ± 0.2	—	3.6 ± 0.2	—
5	—	—	—	3.6 ± 0.2
6	3.7 ± 0.2	3.5 ± 0.2	3.5 ± 0.2	4.0 ± 0.2
7	—	—	—	—
8	—	—	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 18 for enzyme genotypes.

Family[a]					
14-2	14-4	14-5	15-1	15-2	9-3
3.5 ± 0.2	—	—	4.6 ± 0.1	4.1 ± 0.2	2.9 ± 0.2
—	—	—	4.5 ± 0.1	4.7 ± 0.1	—
3.9 ± 0.2	4.2 ± 0.1	4.2 ± 0.1	4.7 ± 0.1	4.5 ± 0.1	3.5 ± 0.2
—	—	—	4.5 ± 0.1	4.2 ± 0.2	—
3.7 ± 0.1	—	—	4.4 ± 0.1	—	—
3.6 ± 0.2	—	—	—	—	—
3.9 ± 0.3	—	—	4.5 ± 0.1	4.6 ± 0.1	3.0 ± 0.2
4.1 ± 0.1	—	—	4.6 ± 0.1	—	—
—	—	—	4.5 ± 0.1	—	—

Table 56. Means and standard errors for plant type for families within each enzyme locus genotype in the 1-locus class for Cross 2 averaged over two locations

Enzyme locus genotype[b]	Family[a]			
	11-1	11-2	11-4	14-1
0	3.1 ± 0.3	3.0 ± 0.2	3.1 ± 0.3	3.1 ± 0.3
1	—	—	—	—
2	3.1 ± 0.2	3.2 ± 0.3	3.0 ± 0.2	—
3	—	—	—	—
4	3.7 ± 0.3	—	3.5 ± 0.2	3.1 ± 0.2
5	—	—	—	3.6 ± 0.3
6	2.9 ± 0.2	3.0 ± 0.3	3.3 ± 0.3	3.5 ± 0.3
7	—	—	—	—
8	—	—	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 18 for enzyme genotypes.

Family[a]					
14-2	14-4	14-5	15-1	15-2	9-3
3.2 ± 0.2	—	—	4.4 ± 0.2	3.5 ± 0.4	2.7 ± 0.3
—	—	—	4.5 ± 0.2	4.8 ± 0.1	—
3.6 ± 0.2	4.0 ± 0.2	4.1 ± 0.2	4.7 ± 0.2	4.4 ± 0.2	2.7 ± 0.2
—	—	—	4.6 ± 0.1	3.8 ± 0.3	—
3.4 ± 0.2	—	—	3.7 ± 0.2	—	—
3.7 ± 0.2	—	—	—	—	—
3.5 ± 0.6	—	—	4.2 ± 0.2	4.8 ± 0.1	2.3 ± 0.3
3.9 ± 0.2	—	—	4.6 ± 0.2	—	—
—	—	—	4.2 ± 0.2	—	—

Table 57. Means and standard errors for vining for families within each enzyme locus genotype in the 1-locus class for Cross 2 averaged over two locations

Enzyme locus genotype[b]	Family[a]			
	11-1	11-2	11-4	14-1
0	2.3 ± 0.2	2.4 ± 0.2	2.8 ± 0.2	2.2 ± 0.2
1	—	—	—	—
2	2.3 ± 0.2	2.4 ± 0.2	2.7 ± 0.2	—
3	—	—	—	—
4	2.3 ± 0.2	—	2.8 ± 0.2	1.9 ± 0.2
5	—	—	—	2.4 ± 0.2
6	2.0 ± 0.2	2.2 ± 0.2	2.7 ± 0.2	2.6 ± 0.2
7	—	—	—	—
8	—	—	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 18 for enzyme genotypes.

Family[a]					
14-2	14-4	14-5	15-1	15-2	9-3
2.3 ± 0.2	—	—	4.1 ± 0.2	3.0 ± 0.2	2.3 ± 0.3
—	—	—	3.9 ± 0.2	4.1 ± 0.2	—
2.7 ± 0.1	3.5 ± 0.2.	3.6 ± 0.2	4.2 ± 0.2	3.8 ± 0.2	2.4 ± 0.2
—	—	—	4.1 ± 0.1	3.2 ± 0.2	—
2.4 ± 0.1	—	—	3.2 ± 0.2	—	—
2.5 ± 0.2	—	—	—	—	—
2.0 ± 0.4	—	—	3.7 ± 0.2	4.2 ± 0.1	2.0 ± 0.2
2.7 ± 0.2	—	—	4.0 ± 0.1	—	—
—	—	—	3.8 ± 0.2	—	—

Table 58. Means and standard errors for date of maturity for families within each enzyme locus genotype in the 2-locus class for Cross 2 averaged over two locations

Enzyme locus genotype[b]	Family[a]									
	11-1	11-2	11-4	14-1	14-2	14-4	14-5	15-1	15-2	9-3
0	17 ± 1	18 ± 1	29 ± 1	15 ± 1	15 ± 1	—	—	26 ± 1	29 ± 3	27 ± 2
12	—	—	—	—	—	—	31 ± 2	—	—	—
13	—	—	—	—	—	—	—	32 ± 1	19 ± 2	—
14	—	—	—	—	—	—	—	20 ± 2	27 ± 3	—
15	—	—	—	15 ± 2	—	—	—	—	—	—
16	—	—	—	—	—	—	—	27 ± 2	38 ± 3	—
17	—	—	—	—	—	—	—	25 ± 1	—	—
23	—	—	—	—	—	—	—	—	31 ± 1	—
24	10 ± 0	—	17 ± 1	—	10 ± 1	24 ± 2	30 ± 1	22 ± 2	25 ± 1	—
25	—	—	—	—	14 ± 2	26 ± 1	30 ± 1	—	—	—
26	18 ± 1	18 ± 1	19 ± 2	18 ± 3	—	26 ± 5	34 ± 5	22 ± 2	46 ± 1	25 ± 2
27	—	—	—	—	17 ± 1	—	—	—	—	—
28	—	—	—	—	—	17 ± 2	—	23 ± 1	—	—
34	—	—	—	—	—	—	—	21 ± 1	20 ± 3	—
36	—	—	—	—	—	—	—	27 ± 1	39 ± 2	—
37	—	—	—	—	—	—	—	21 ± 2	—	—
45	—	—	—	14 ± 1	8 ± 1	—	—	—	—	—
46	11 ± 1	—	22 ± 1	13 ± 1	—	—	—	7 ± 1	25 ± 2	—
47	—	—	—	—	11 ± 1	—	—	18 ± 2	—	—
56	—	—	—	14 ± 1	—	—	—	—	—	—
57	—	—	—	—	11 ± 2	—	—	—	—	—
67	—	—	—	—	—	—	—	38 ± 2	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 18 for enzyme genotypes.

Table 59. Means and standard errors for height for families within each enzyme locus genotype in the 2-locus class for Cross 2 averaged over two locations

Enzyme locus genotype[b]	Family[a]									
	11-1	11-2	11-4	14-1	14-2	14-4	14-5	15-1	15-2	9-3
0	77 ± 4	83 ± 3	119 ± 4	66 ± 2	73 ± 5	—	—	126 ± 6	105 ± 7	87 ± 2
12	—	—	—	—	—	—	120 ± 4	—	—	—
13	—	—	—	—	—	—	—	135 ± 5	106 ± 5	—
14	—	—	—	—	—	—	—	106 ± 4	121 ± 7	—
15	—	—	—	60 ± 4	—	—	—	—	—	—
16	—	—	—	—	—	—	—	128 ± 7	149 ± 7	—
17	—	—	—	—	—	—	—	127 ± 4	—	—
23	—	—	—	—	—	—	—	—	145 ± 7	—
24	72 ± 3	—	97 ± 6	—	60 ± 3	101 ± 4	113 ± 5	125 ± 14	125 ± 4	—
25	—	—	—	—	63 ± 3	94 ± 5	96 ± 3	—	—	—
26	77 ± 2	77 ± 2	88 ± 4	66 ± 6	—	105 ± 11	124 ± 12	125 ± 5	136 ± 8	90 ± 3
27	—	—	—	—	76 ± 3	—	—	—	—	—
28	—	—	—	—	—	74 ± 3	—	106 ± 5	—	—
34	—	—	—	—	—	—	—	97 ± 4	108 ± 4	—
36	—	—	—	—	—	—	—	121 ± 4	141 ± 7	—
37	—	—	—	—	—	—	—	108 ± 4	—	—
45	—	—	—	61 ± 2	64 ± 3	—	—	—	—	—
46	68 ± 2	—	109 ± 4	75 ± 2	—	—	—	81 ± 5	112 ± 7	—
47	—	—	—	—	66 ± 2	—	—	99 ± 9	—	—
56	—	—	—	63 ± 3	—	—	—	—	—	—
57	—	—	—	—	71 ± 3	—	—	—	—	—
67	—	—	—	—	—	—	—	121 ± 5	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 18 for enzyme genotypes.

Table 60. Means and standard errors for lodging for families within each enzyme locus genotype in the 2-locus class for Cross 2 averaged over two locations

Enzyme locus genotype[b]	Family[a]			
	11-1	11-2	11-4	14-1
0	3.7 ± 0.2	3.6 ± 0.2	3.8 ± 0.2	3.0 ± 0.2
12	—	—	—	—
13	—	—	—	—
14	—	—	—	—
15	—	—	—	3.4 ± 0.3
16	—	—	—	—
17	—	—	—	—
23	—	—	—	—
24	3.6 ± 0.2	—	3.7 ± 0.2	—
25	—	—	—	—
26	3.4 ± 0.1	3.1 ± 0.3	3.2 ± 0.2	4.0 ± 0.2
27	—	—	—	—
28	—	—	—	—
34	—	—	—	—
36	—	—	—	—
37	—	—	—	—
45	—	—	—	3.4 ± 0.2
46	3.2 ± 0.2	—	3.4 ± 0.2	3.6 ± 0.2
47	—	—	—	—
56	—	—	—	3.5 ± 0.2
57	—	—	—	—
67	—	—	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 18 for enzyme genotypes.

Family[a]					
14-2	14-4	14-5	15-1	15-2	9-3
3.5 ± 0.2	—	—	4.6 ± 0.1	4.1 ± 0.2	2.9 ± 0.2
—	—	4.3 ± 0.1	—	—	—
—	—	—	4.8 ± 0.1	4.8 ± 0.1	—
—	—	—	4.5 ± 0.1	4.4 ± 0.2	—
—	—	—	—	—	—
—	—	—	4.7 ± 0.1	4.6 ± 0.1	—
—	—	—	4.6 ± 0.1	—	—
—	—	—	—	4.7 ± 0.1	—
3.4 ± 0.2	4.0 ± 0.2	4.2 ± 0.1	4.9 ± 0.1	4.7 ± 0.1	—
3.6 ± 0.2	4.0 ± 0.1	3.8 ± 0.1	—	—	—
—	4.1 ± 0.2	4.5 ± 0.1	4.7 ± 0.1	4.5 ± 0.1	3.0 ± 0.2
4.1 ± 0.1	—	—	—	—	—
—	4.1 ± 0.1	—	4.4 ± 0.1	—	—
—	—	—	4.6 ± 0.1	4.5 ± 0.2	—
—	—	—	4.5 ± 0.1	4.4 ± 0.1	—
—	—	—	4.7 ± 0.1	—	—
3.9 ± 0.2	—	—	—	—	—
—	—	—	4.6 ± 0.1	4.4 ± 0.1	—
3.8 ± 0.1	—	—	4.7 ± 0.1	—	—
—	—	—	—	—	—
4.0 ± 0.2	—	—	—	—	—
—	—	—	4.6 ± 0.1	—	—

Table 61. Means and standard errors for plant type for families within each enzyme locus genotype in the 2-locus class for Cross 2 averaged over two locations

Enzyme locus genotype[b]	Family[a] 11-1	11-2	11-4	14-1
0	3.1 ± 0.3	3.0 ± 0.2	3.1 ± 0.3	3.1 ± 0.3
12	—	—	—	—
13	—	—	—	—
14	—	—	—	—
15	—	—	—	2.4 ± 0.3
16	—	—	—	—
17	—	—	—	—
23	—	—	—	—
24	3.6 ± 0.2	—	3.6 ± 0.3	—
25	—	—	—	—
26	2.9 ± 0.3	3.2 ± 0.3	3.0 ± 0.2	3.6 ± 0.3
27	—	—	—	—
28	—	—	—	—
34	—	—	—	—
36	—	—	—	—
37	—	—	—	—
45	—	—	—	3.4 ± 0.2
46	3.3 ± 0.2	—	3.3 ± 0.2	3.2 ± 0.3
47	—	—	—	—
56	—	—	—	3.4 ± 0.3
57	—	—	—	—
67	—	—	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 18 for enzyme genotypes.

Family[a]					
14-2	14-4	14-5	15-1	15-2	9-3
3.2 ± 0.2	—	—	4.4 ± 0.2	3.5 ± 0.4	2.7 ± 0.3
—	—	4.4 ± 0.2	—	—	—
—	—	—	4.9 ± 0.1	4.6 ± 0.3	—
—	—	—	4.2 ± 0.2	4.0 ± 0.3	—
—	—	—	—	—	—
—	—	—	4.4 ± 0.2	4.8 ± 0.3	—
—	—	—	4.5 ± 0.2	—	—
—	—	—	—	4.3 ± 0.3	—
3.0 ± 0.3	3.9 ± 0.3	4.1 ± 0.2	4.4 ± 0.4	4.6 ± 0.3	—
3.6 ± 0.2	3.8 ± 0.2	3.4 ± 0.2	—	—	—
—	4.4 ± 0.2	4.4 ± 0.4	4.7 ± 0.2	4.4 ± 0.2	2.8 ± 0.2
3.5 ± 0.3	—	—	—	—	—
—	3.7 ± 0.2	—	4.0 ± 0.3	—	—
—	—	—	4.2 ± 0.2	4.3 ± 0.3	—
—	—	—	4.6 ± 0.2	4.3 ± 0.2	—
—	—	—	4.6 ± 0.2	—	—
3.7 ± 0.2	—	—	—	—	—
—	—	—	4.1 ± 0.2	4.2 ± 0.3	—
—	—	—	4.5 ± 0.2	—	—
—	—	—	—	—	—
3.5 ± 0.3	—	—	—	—	—
—	—	—	4.6 ± 0.2	—	—

Table 62. Means and standard errors for vining for families within each enzyme locus genotype in the 2-locus class for Cross 2 averaged over two locations

Enzyme locus genotype[b]	Family[a]			
	11-1	11-2	11-4	14-1
0	2.3 ± 0.2	2.4 ± 0.2	2.8 ± 0.2	2.2 ± 0.2
12	—	—	—	—
13	—	—	—	—
14	—	—	—	—
15	—	—	—	1.5 ± 0.3
16	—	—	—	—
17	—	—	—	—
23	—	—	—	—
24	2.5 ± 0.2	—	2.9 ± 0.2	—
25	—	—	—	—
26	2.4 ± 0.2	2.1 ± 0.2	2.4 ± 0.1	2.6 ± 0.3
27	—	—	—	—
28	—	—	—	—
34	—	—	—	—
36	—	—	—	—
37	—	—	—	—
45	—	—	—	2.2 ± 0.1
46	2.1 ± 0.2	—	2.7 ± 0.2	2.3 ± 0.2
47	—	—	—	—
56	—	—	—	2.5 ± 0.2
57	—	—	—	—
67	—	—	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 18 for enzyme genotypes.

Family[a]					
14-2	14-4	14-5	15-1	15-2	9-3
2.3 ± 0.2	—	—	4.1 ± 0.2	3.0 ± 0.2	2.3 ± 0.3
—	—	3.8 ± 0.2	—	—	—
—	—	—	4.7 ± 0.1	4.0 ± 0.3	—
—	—	—	3.8 ± 0.2	3.6 ± 0.4	—
—	—	—	—	—	—
—	—	—	3.8 ± 0.3	4.4 ± 0.3	—
—	—	—	4.2 ± 0.2	—	—
—	—	—	—	4.3 ± 0.3	—
2.0 ± 0.2	3.4 ± 0.3	3.4 ± 0.2	3.9 ± 0.4	3.9 ± 0.3	—
2.4 ± 0.2	3.3 ± 0.2	2.8 ± 0.2	—	—	—
—	3.4 ± 0.3	3.4 ± 0.3	3.7 ± 0.2	4.0 ± 0.2	2.3 ± 0.2
2.7 ± 0.2	—	—	—	—	—
—	2.9 ± 0.2	—	3.4 ± 0.2	—	—
—	—	—	3.8 ± 0.3	3.6 ± 0.4	—
—	—	—	4.2 ± 0.2	3.9 ± 0.2	—
—	—	—	4.1 ± 0.2	—	—
2.7 ± 0.2	—	—	—	—	—
—	—	—	3.1 ± 0.2	3.4 ± 0.3	—
2.2 ± 0.2	—	—	3.9 ± 0.2	—	—
—	—	—	—	—	—
2.5 ± 0.1	—	—	—	—	—
—	—	—	4.4 ± 0.1	—	—

Table 63. Means and standard errors for date of maturity for families within each enzyme locus genotype in the 3-locus class for Cross 2 averaged over two locations

Enzyme locus genotype[b]	Family[a]									
	11-1	11-2	11-4	14-1	14-2	14-4	14-5	15-1	15-2	9-3
0	17 ± 1	18 ± 1	29 ± 1	15 ± 1	15 ± 1	—	—	26 ± 1	29 ± 3	27 ± 2
124	—	—	—	—	—	—	29 ± 1	—	—	—
125	—	—	—	—	—	—	25 ± 2	—	—	—
126	—	—	18 ± 2	—	—	—	—	—	39 ± 2	—
134	—	—	—	—	—	—	—	22 ± 1	—	—
136	—	—	—	—	—	—	—	29 ± 2	37 ± 2	—
137	—	—	—	—	—	—	—	34 ± 2	—	—
147	14 ± 2	—	—	—	—	—	—	16 ± 1	—	—
167	—	—	—	—	—	—	—	27 ± 2	—	—
234	—	—	—	—	—	—	—	—	26 ± 1	—
236	—	—	—	—	—	—	—	—	39 ± 1	—
245	—	—	—	—	9 ± 1	14 ± 2	25 ± 2	—	—	—
246	15 ± 1	—	23 ± 1	—	—	28 ± 1	—	—	31 ± 1	21 ± 1
247	—	—	—	—	12 ± 1	—	—	—	—	—
248	—	—	—	—	—	23 ± 2	—	19 ± 2	—	—
256	—	—	—	—	—	40 ± 1	—	—	—	—
257	—	—	—	—	15 ± 2	—	—	—	—	—
258	—	—	—	—	—	26 ± 3	—	—	—	—
268	—	—	—	—	—	33 ± 2	—	—	—	—
346	—	—	—	—	—	—	—	24 ± 2	33 ± 1	—
347	—	—	—	—	—	—	—	22 ± 2	—	—
367	—	—	—	—	—	—	—	30 ± 2	—	—
456	—	—	—	8 ± 1	—	—	—	—	—	—
457	—	—	—	—	11 ± 1	—	—	—	—	—
467	—	—	—	—	—	—	—	24 ± 1	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 18 for enzyme genotypes.

Table 64. Means and standard errors for height for families within each enzyme locus genotype in the 3-locus class for Cross 2 averaged over two locations

Enzyme locus genotype[b]	Family[a]									
	11-1	11-2	11-4	14-1	14-2	14-4	14-5	15-1	15-2	9-3
0	77 ± 4	83 ± 3	119 ± 4	66 ± 2	73 ± 5	—	—	126 ± 6	105 ± 7	87 ± 2
124	—	—	—	—	—	—	103 ± 2	—	—	—
125	—	—	—	—	—	—	102 ± 5	—	—	—
126	—	—	90 ± 6	—	—	—	—	—	144 ± 8	—
134	—	—	—	—	—	—	—	112 ± 6	—	—
136	—	—	—	—	—	—	—	131 ± 3	121 ± 14	—
137	—	—	—	—	—	—	—	149 ± 5	—	—
147	81 ± 4	—	—	—	—	—	—	105 ± 6	—	—
167	—	—	—	—	—	—	—	133 ± 5	—	—
234	—	—	—	—	—	—	—	—	105 ± 7	—
236	—	—	—	—	—	—	—	—	149 ± 8	—
245	—	—	—	—	63 ± 6	72 ± 2	88 ± 2	—	—	—
246	69 ± 3	—	108 ± 6	—	—	103 ± 4	—	—	137 ± 4	87 ± 6
247	—	—	—	—	70 ± 2	—	—	—	—	—
248	—	—	—	—	—	75 ± 4	—	111 ± 7	—	—
256	—	—	—	—	—	126 ± 5	—	—	—	—
257	—	—	—	—	68 ± 3	—	—	—	—	—
258	—	—	—	—	—	86 ± 5	—	—	—	—
268	—	—	—	—	—	98 ± 4	—	—	—	—
346	—	—	—	—	—	—	—	119 ± 6	140 ± 3	—
347	—	—	—	—	—	—	—	121 ± 4	—	—
367	—	—	—	—	—	—	—	125 ± 4	—	—
456	—	—	—	62 ± 2	—	—	—	—	—	—
457	—	—	—	—	69 ± 3	—	—	—	—	—
467	—	—	—	—	—	—	—	121 ± 5	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 18 for enzyme genotypes.

Table 65. Means and standard errors for lodging for families within each enzyme locus genotype in the 3-locus class for Cross 2 averaged over two locations

Enzyme locus genotype[b]	Family[a]			
	11-1	11-2	11-4	14-1
0	3.7 ± 0.2	3.6 ± 0.2	3.8 ± 0.2	3.0 ± 0.2
124	—	—	—	—
125	—	—	—	—
126	—	—	4.0 ± 0.2	—
134	—	—	—	—
136	—	—	—	—
137	—	—	—	—
147	4.5 ± 0.1	—	—	—
167	—	—	—	—
234	—	—	—	—
236	—	—	—	—
245	—	—	—	—
246	3.1 ± 0.2	—	3.5 ± 0.2	—
247	—	—	—	—
248	—	—	—	—
256	—	—	—	—
257	—	—	—	—
258	—	—	—	—
268	—	—	—	—
346	—	—	—	—
347	—	—	—	—
367	—	—	—	—
456	—	—	—	3.5 ± 0.2
457	—	—	—	—
467	—	—	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 18 for enzyme genotypes.

Family[a]					
14-2	14-4	14-5	15-1	15-2	9-3
3.5 ± 0.2	—	—	4.6 ± 0.1	4.1 ± 0.2	2.9 ± 0.2
—	—	4.2 ± 0.1	—	—	—
—	—	4.1 ± 0.2	—	—	—
—	—	—	—	4.4 ± 0.1	—
—	—	—	4.7 ± 0.1	—	—
—	—	—	4.5 ± 0.1	4.4 ± 0.2	—
—	—	—	4.5 ± 0.1	—	—
—	—	—	4.6 ± 0.1	—	—
—	—	—	4.8 ± 0.1	—	—
—	—	—	—	4.2 ± 0.1	—
—	—	—	—	4.5 ± 0.1	—
3.5 ± 0.2	4.0 ± 0.2	4.1 ± 0.1	—	—	—
3.8 ± 0.2	4.3 ± 0.2	—	—	4.6 ± 0.1	3.3 ± 0.2
—	—	—	—	—	—
—	3.8 ± 0.2	—	4.6 ± 0.1	—	—
3.6 ± 0.1	4.2 ± 0.1	—	—	—	—
—	—	—	—	—	—
—	3.7 ± 0.2	—	—	—	—
—	4.2 ± 0.1	—	—	—	—
—	—	—	4.6 ± 0.1	4.5 ± 0.1	—
—	—	—	4.4 ± 0.1	—	—
—	—	—	4.6 ± 0.1	—	—
—	—	—	—	—	—
3.7 ± 0.2	—	—	—	—	—
—	—	—	4.5 ± 0.1	—	—

Table 66. Means and standard errors for plant type for families within each enzyme locus genotype in the 3-locus class for Cross 2 averaged over two locations

Enzyme locus genotype[b]	Family[a]			
	11-1	11-2	11-4	14-1
0	3.1 ± 0.3	3.0 ± 0.2	3.1 ± 0.3	3.1 ± 0.3
124	—	—	—	—
125	—	—	—	—
126	—	—	2.9 ± 0.4	—
134	—	—	—	—
136	—	—	—	—
137	—	—	—	—
147	3.5 ± 0.4	—	—	—
167	—	—	—	—
234	—	—	—	—
236	—	—	—	—
245	—	—	—	—
246	3.0 ± 0.2	—	3.0 ± 0.3	—
247	—	—	—	—
248	—	—	—	—
256	—	—	—	—
257	—	—	—	—
258	—	—	—	—
268	—	—	—	—
346	—	—	—	—
347	—	—	—	—
367	—	—	—	—
456	—	—	—	3.4 ± 0.3
457	—	—	—	—
467	—	—	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 18 for enzyme genotypes.

Family[a]					
14-2	14-4	14-5	15-1	15-2	9-3
3.2 ± 0.2	—	—	4.4 ± 0.2	3.5 ± 0.4	2.7 ± 0.3
—	—	3.5 ± 0.2	—	—	—
—	—	3.8 ± 0.2	—	—	—
—	—	—	—	4.2 ± 0.2	—
—	—	—	4.4 ± 0.2	—	—
—	—	—	4.4 ± 0.2	4.5 ± 0.3	—
—	—	—	4.7 ± 0.2	—	—
—	—	—	4.2 ± 0.2	—	—
—	—	—	4.6 ± 0.2	—	—
—	—	—	—	3.6 ± 0.2	—
—	—	—	—	4.6 ± 0.2	—
3.4 ± 0.2	3.5 ± 0.2	3.5 ± 0.1	—	—	—
—	4.2 ± 0.2	—	—	4.7 ± 0.2	3.0 ± 0.3
3.3 ± 0.2	—	—	—	—	—
—	3.6 ± 0.3	—	4.8 ± 0.2	—	—
—	4.2 ± 0.2	—	—	—	—
3.4 ± 0.2	—	—	—	—	—
—	3.6 ± 0.3	—	—	—	—
—	3.9 ± 0.2	—	—	—	—
—	—	—	4.5 ± 0.2	4.4 ± 0.2	—
—	—	—	4.3 ± 0.2	—	—
—	—	—	4.5 ± 0.2	—	—
—	—	—	—	—	—
3.2 ± 0.2	—	—	—	—	—
—	—	—	4.2 ± 0.2	—	—

Table 67. Means and standard errors for vining for families within each enzyme locus genotype in the 3-locus class for Cross 2 averaged over two locations

Enzyme locus genotype[b]	Family[a]			
	11-1	11-2	11-4	14-1
0	2.3 ± 0.2	2.4 ± 0.2	2.8 ± 0.2	2.2 ± 0.2
124	—	—	—	—
125	—	—	—	—
126	—	—	2.5 ± 0.3	—
134	—	—	—	—
136	—	—	—	—
137	—	—	—	—
147	2.3 ± 0.3	—	—	—
167	—	—	—	—
234	—	—	—	—
236	—	—	—	—
245	—	—	—	—
246	2.2 ± 0.2	—	2.6 ± 0.2	—
247	—	—	—	—
248	—	—	—	—
256	—	—	—	—
257	—	—	—	—
258	—	—	—	—
268	—	—	—	—
346	—	—	—	—
347	—	—	—	—
367	—	—	—	—
456	—	—	—	2.1 ± 0.2
457	—	—	—	—
467	—	—	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 18 for enzyme genotypes.

Family[a]					
14-2	14-4	14-5	15-1	15-2	9-3
2.3 ± 0.2	—	—	4.1 ± 0.2	3.0 ± 0.2	2.3 ± 0.3
—	—	3.1 ± 0.2	—	—	—
—	—	3.0 ± 0.2	—	—	—
—	—	—	—	3.9 ± 0.2	—
—	—	—	4.1 ± 0.2	—	—
—	—	—	4.0 ± 0.2	4.3 ± 0.3	—
—	—	—	4.6 ± 0.2	—	—
—	—	—	3.5 ± 0.2	—	—
—	—	—	4.6 ± 0.2	—	—
—	—	—	—	3.2 ± 0.2	—
—	—	—	—	4.4 ± 0.2	—
2.0 ± 0.1	2.7 ± 0.2	3.1 ± 0.1	—	—	—
—	3.6 ± 0.2	—	—	4.5 ± 0.1	2.4 ± 0.2
2.3 ± 0.2	—	—	—	—	—
—	2.7 ± 0.2	—	4.1 ± 0.2	—	—
—	3.6 ± 0.2	—	—	—	—
2.3 ± 0.2	—	—	—	—	—
—	2.9 ± 0.2	—	—	—	—
—	3.2 ± 0.2	—	—	—	—
—	—	—	4.2 ± 0.2	4.4 ± 0.1	—
—	—	—	3.6 ± 0.2	—	—
—	—	—	4.1 ± 0.2	—	—
—	—	—	—	—	—
2.3 ± 0.1	—	—	—	—	—
—	—	—	3.7 ± 0.2	—	—

Table 68. Means and standard errors for date of maturity for families within each enzyme locus genotype in the 4-locus class for Cross 2 averaged over two locations

Enzyme locus genotype[b]	Family[a]									
	11-1	11-2	11-4	14-1	14-2	14-4	14-5	15-1	15-2	9-3
0	17 ± 1	18 ± 1	29 ± 1	15 ± 1	15 ± 1	—	—	26 ± 1	29 ± 3	27 ± 2
1245	—	—	—	—	—	—	15 ± 1	—	—	—
1246	—	—	—	—	—	—	—	—	31 ± 2	—
1367	—	—	—	—	—	—	—	27 ± 1	—	—
1467	17 ± 3	—	—	—	—	—	—	14 ± 1	—	—
2368	—	—	—	—	17 ± 1	—	—	—	—	—
2456	—	—	—	—	—	23 ± 2	—	—	—	—
2457	—	—	—	—	9 ± 1	—	—	—	—	—
2458	—	—	—	—	—	25 ± 1	—	—	—	—
2468	—	—	—	—	—	22 ± 2	—	—	—	—
2568	—	—	—	—	—	39 ± 1	—	—	—	—
3467	—	—	—	—	—	—	—	19 ± 1	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 18 for enzyme genotypes.

Table 69. Means and standard errors for height for families within each enzyme locus genotype in the 4-locus class for Cross 2 averaged over two locations

Enzyme locus genotype[b]	Family[a]									
	11-1	11-2	11-4	14-1	14-2	14-4	14-5	15-1	15-2	9-3
0	77 ± 4	83 ± 3	119 ± 4	66 ± 2	73 ± 5	—	—	126 ± 6	105 ± 7	87 ± 2
1245	—	—	—	—	—	—	78 ± 6	—	—	—
1246	—	—	—	—	—	—	—	—	118 ± 5	—
1367	—	—	—	—	—	—	—	120 ± 5	—	—
1467	82 ± 5	—	—	—	—	—	—	111 ± 4	—	—
2368	—	—	—	—	87 ± 2	—	—	—	—	—
2456	—	—	—	—	—	92 ± 6	—	—	—	—
2457	—	—	—	—	64 ± 3	—	—	—	—	—
2458	—	—	—	—	—	93 ± 7	—	—	—	—
2468	—	—	—	—	—	89 ± 3	—	—	—	—
2568	—	—	—	—	—	116 ± 6	—	—	—	—
3467	—	—	—	—	—	—	—	103 ± 5	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 18 for enzyme genotypes.

Table 70. Means and standard errors for lodging for families within each enzyme locus genotype in the 4-locus class for Cross 2 averaged over two locations

Enzyme locus genotype[b]	Family[a]			
	11-1	11-2	11-4	14-1
0	3.7 ± 0.2	3.6 ± 0.2	3.8 ± 0.2	3.0 ± 0.2
1245	—	—	—	—
1246	—	—	—	—
1367	—	—	—	—
1467	4.3 ± 0.2	—	—	—
2368	—	—	—	—
2456	—	—	—	—
2457	—	—	—	—
2458	—	—	—	—
2468	—	—	—	—
2568	—	—	—	—
3467	—	—	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 18 for enzyme genotypes.

Family[a]					
14-2	14-4	14-5	15-1	15-2	9-3
3.5 ± 0.2	—	—	4.6 ± 0.1	4.1 ± 0.2	2.9 ± 0.2
—	—	4.2 ± 0.1	—	—	—
—	—	—	—	4.2 ± 0.2	—
—	—	—	4.7 ± 0.1	—	—
—	—	—	4.6 ± 0.1	—	—
4.0 ± 0.2	—	—	—	—	—
4.1 ± 0.2	3.9 ± 0.2	—	—	—	—
—	—	—	—	—	—
—	4.1 ± 0.2	—	—	—	—
—	4.3 ± 0.1	—	—	—	—
—	4.1 ± 0.1	—	—	—	—
—	—	—	4.8 ± 0.1	—	—

Table 71. Means and standard errors for plant type for families within each enzyme locus genotype in the 4-locus class for Cross 2 averaged over two locations

Enzyme locus genotype[b]	Family[a]			
	11-1	11-2	11-4	14-1
0	3.1 ± 0.3	3.0 ± 0.2	3.1 ± 0.3	3.1 ± 0.3
1245	—	—	—	—
1246	—	—	—	—
1367	—	—	—	—
1467	3.8 ± 0.4	—	—	—
2368	—	—	—	—
2456	—	—	—	—
2457	—	—	—	—
2458	—	—	—	—
2468	—	—	—	—
2568	—	—	—	—
3467	—	—	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 18 for enzyme genotypes.

Family[a]					
14-2	14-4	14-5	15-1	15-2	9-3
3.2 ± 0.2	—	—	4.4 ± 0.2	3.5 ± 0.4	2.7 ± 0.3
—	—	3.9 ± 0.2	—	—	—
—	—	—	—	4.2 ± 0.3	—
—	—	—	4.5 ± 0.2	—	—
—	—	—	3.7 ± 0.2	—	—
3.4 ± 0.2	—	—	—	—	—
3.6 ± 0.3	4.0 ± 0.2	—	—	—	—
—	—	—	—	—	—
—	4.2 ± 0.2	—	—	—	—
—	3.8 ± 0.2	—	—	—	—
—	4.1 ± 0.2	—	—	—	—
—	—	—	4.2 ± 0.2	—	—

Table 72. Means and standard errors for vining for families within each enzyme locus genotype in the 4-locus class for Cross 2 averaged over two locations

Enzyme locus genotype[b]	Family[a]			
	11-1	11-2	11-4	14-1
0	2.3 ± 0.2	2.4 ± 0.2	2.8 ± 0.2	2.2 ± 0.2
1245	—	—	—	—
1246	—	—	—	—
1367	—	—	—	—
1467	3.3 ± 0.3	—	—	—
2368	—	—	—	—
2456	—	—	—	—
2457	—	—	—	—
2458	—	—	—	—
2468	—	—	—	—
2568	—	—	—	—
3467	—	—	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 18 for enzyme genotypes.

Family[a]					
14-2	14-4	14-5	15-1	15-2	9-3
2.3 ± 0.2	—	—	4.1 ± 0.2	3.0 ± 0.2	2.3 ± 0.3
—	—	2.7 ± 0.2	—	—	—
—	—	—	—	3.6 ± 0.3	—
—	—	—	4.2 ± 0.2	—	—
—	—	—	3.4 ± 0.3	—	—
2.4 ± 0.1	—	—	—	—	—
2.3 ± 0.2	3.2 ± 0.2	—	—	—	—
—	—	—	—	—	—
—	3.6 ± 0.2	—	—	—	—
—	3.2 ± 0.2	—	—	—	—
—	3.8 ± 0.2	—	—	—	—
—	—	—	3.6 ± 0.2	—	—

Table 73. Means and standard errors for date of maturity for families within each enzyme locus genotype in the 5-locus class for Cross 2 averaged over two locations

Enzyme locus genotype[b]	Family[a]									
	11-1	11-2	11-4	14-1	14-2	14-4	14-5	15-1	15-2	9-3
0	17 ± 1	18 ± 1	29 ± 1	15 ± 1	15 ± 1	—	—	26 ± 1	29 ± 3	27 ± 2
12346	—	—	—	—	—	—	—	—	35 ± 2	—
13467	—	—	—	—	—	—	—	18 ± 1	—	—
23468	—	—	—	—	20 ± 1	—	—	—	—	—
24568	—	—	—	—	—	29 ± 1	—	—	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 18 for enzyme genotypes.

Table 74. Means and standard errors for height for families within each enzyme locus genotype in the 5-locus class for Cross 2 averaged over two locations

Enzyme locus genotype[b]	Family[a]									
	11-1	11-2	11-4	14-1	14-2	14-4	14-5	15-1	15-2	9-3
0	77 ± 4	83 ± 3	119 ± 4	66 ± 2	73 ± 5	—	—	126 ± 6	105 ± 7	87 ± 2
12346	—	—	—	—	—	—	—	—	145 ± 5	—
13467	—	—	—	—	—	—	—	115 ± 5	—	—
23468	—	—	—	—	90 ± 3	—	—	—	—	—
24568	—	—	—	—	—	102 ± 6	—	—	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 18 for enzyme genotypes.

Table 75. Means and standard errors for lodging for families within each enzyme locus genotype in the 5-locus class for Cross 2 averaged over two locations

Enzyme locus genotype[b]	Family[a]			
	11-1	11-2	11-4	14-1
0	3.7 ± 0.2	3.6 ± 0.2	3.8 ± 0.2	3.0 ± 0.2
12346	—	—	—	—
13467	—	—	—	—
23468	—	—	—	—
24568	—	—	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 18 for enzyme genotypes.

Family[a]					
14-2	14-4	14-5	15-1	15-2	9-3
3.5 ± 0.2	—	—	4.6 ± 0.1	4.1 ± 0.2	2.9 ± 0.2
—	—	—	—	4.6 ± 0.1	—
—	—	—	4.6 ± 0.1	—	—
3.6 ± 0.2	—	—	—	—	—
—	4.6 ± 0.1	—	—	—	—

Table 76. Means and standard errors for plant type for families within each enzyme locus genotype in the 5-locus class for Cross 2 averaged over two locations

Enzyme locus genotype[b]	Family[a]			
	11-1	11-2	11-4	14-1
0	3.1 ± 0.3	3.0 ± 0.2	3.1 ± 0.3	3.1 ± 0.3
12346	—	—	—	—
13467	—	—	—	—
23468	—	—	—	—
24568	—	—	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 18 for enzyme genotypes.

Family[a]					
14-2	14-4	14-5	15-1	15-2	9-3
3.2 ± 0.2	—	—	4.4 ± 0.2	3.5 ± 0.4	2.7 ± 0.3
—	—	—	—	4.4 ± 0.2	—
—	—	—	4.3 ± 0.2	—	—
2.6 ± 0.2	—	—	—	—	—
—	4.6 ± 0.2	—	—	—	—

Table 77. Means and standard errors for vining for families within each enzyme locus genotype in the 5-locus class for Cross 2 averaged over two locations

Enzyme locus genotype[b]	Family[a]			
	11-1	11-2	11-4	14-1
0	2.3 ± 0.2	2.4 ± 0.2	2.8 ± 0.2	2.2 ± 0.2
12346	—	—	—	—
13467	—	—	—	—
23468	—	—	—	—
24568	—	—	—	—

[a] BC_2F_4-derived lines whose ancestry traces to the same BC_2F_1 plant.

[b] See Table 18 for enzyme genotypes.

Family[a]					
14-2	14-4	14-5	15-1	15-2	9-3
2.3 ± 0.2	—	—	4.1 ± 0.2	3.0 ± 0.2	2.3 ± 0.3
—	—	—	—	4.5 ± 0.1	—
—	—	—	3.7 ± 0.2	—	—
2.0 ± 0.1	—	—	—	—	—
—	4.1 ± 0.2	—	—	—	—

example, the Pgm1 locus was associated with later maturity in Cross 1 (Table 23). The later maturity relative to the 0 class was observed only in three out of six BC_2F_1 families sampled (Table 33). The family differences implied recombination between the Pgm1 locus and linked genes affecting maturity. No effect on maturity was observed for the Pgm1 locus (genotype 6) in Cross 2 (Table 28). However, when individual family means were examined, for one of the eight families representing genotype 6 in Cross 2, there was an association with later maturity similar to that observed in Cross 1 (Table 53). The Dia1 locus (genotype 4) was associated with large effects on MAT and HT in Cross 2. For MAT, lines that were homozygous for G. soja alleles at the Dia1 locus were earlier in maturity than the 0 class for all five of the families that were sampled (Table 53). This implies either a pleiotropic effect of Dia1-b alleles on maturity or tight linkage with genes that affect maturity. For HT, three out of the five families were shorter than the 0 class, implying recombination between the Dia1 locus and genes that affect plant height (Table 54). Additional examples of family differences exist for all of the traits for the single and multilocus enzyme genotypes for Cross 1 (Tables 33 through 52) and Cross 2 (Tables 53 through 77).

The family means revealed some associations between isozyme loci and quantitative traits that were not evident from the average of all families. For example, in Cross 1, the Idh2 locus was associated with genes affecting maturity, but the average MAT over families indicated an association with earlier maturity (Table 23), while the family means showed an association between Idh2 and later maturity in one of the

three families represented (Table 33). The Ap and Pgm2 loci were associated with genes that affected MAT in some families (Table 33), but the data averaged over families did not reveal these associations (Table 23). The apparent association of Aco2-a homozygotes with earlier MAT (Table 23) could not be separated from a family effect (Table 33). For Cross 2, the effects of the Aco2 and Ap loci on MAT could not be separated from family effects (Table 53). The apparent associations of the Idh1, Ap, and MDH loci with genes that affected plant height were due to family differences, as were the effects of Idh1 and MDH loci on LDG, PLT, and VNG scores. Other genotypes showed effects for some families relative to the 0 class, indicating possible linkage of those loci with genes that influenced the quantitative traits.

Some of the 2-locus genotypes showed effects on the quantitative traits that were similar to one of the loci acting alone. In Cross 1, for example, lines that were homozygous for G. soja alleles at both the Aco2 and Pgi loci (genotype 16) were similar in MAT to lines that had G. soja alleles at only the Aco2 locus (Table 24). Some 2-locus combinations, however, were different than either single-locus genotype alone. For example, the Aco2-a Aco2-a Pgm1-a Pgm1-a genotype had a later maturity and greater plant height than lines that were homozygous for either the Aco2-a or the Pgm1-a alleles alone (Table 24). For Cross 2, the Pgm1-a Pgm1-a Pgm2-b Pgm2-b genotype had a MAT score that was 15 to 17 d later than the 0 class (Table 29). The Pgm1-a Pgm1-a genotype was 2 d later than the 0 class, and the Pgm2-b Pgm2-b genotype showed no effect on MAT (Table 28). The Aco4-b Aco4-b Pgm2-b Pgm2-b genotype was 4 d earlier than the 0 class (Table 28), but the Aco4-b

homozygotes were 4 d later and Pgm2 had no effect (Table 29). The Aco4-Idh1, Aco4-Pgm2, and Pgm1-Pgm2 2-locus combinations showed effects on HT that were different from the effects of either 1-locus genotype alone. For LDG, the Idh1-b Idh1-b Pgm2-b Pgm2-b genotype had a greater score than either the Idh1-b or Pgm2-b homozygotes (Tables 28 and 29). For PLT and VNG, the Aco2-a Aco2-a Ap-a Ap-a genotype had effects that were in the opposite direction of either of the 1-locus genotypes. Both the Aco2-a and the Ap-a homozygotes had PLT and VNG scores greater than the 0 class, but the 2-locus combination had PLT and VNG scores 0.5 lower than the 0 class. The Pgm1-a Pgm1-a Pgm2-b Pgm2-b genotype had PLT and VNG scores that were greater than for either the Pgm1-a or Pgm2-b homozygotes.

Interactions were observed for the 3-, 4-, and 5-locus genotypes in both crosses. For the 3-locus class, many genotypes showed effects that were equal to those of one of the 1- or 2-locus combinations that make up the 3-locus genotype. For example, in Cross 1, the combination of the Aco2, Pgm2, and Pgi loci (genotype 156) had an effect on MAT that was similar to the effect of the Aco2 locus alone or the Aco2-Pgi 2-locus combination (Tables 23 through 25). The effect of the Pgm2 locus was observed in the Pgm2-b homozygotes and in the Aco2-Pgm2 2-locus combination, but not in the Pgm2-Pgi or Aco2-Pgm2-Pgi locus combinations (Tables 23 through 25). For Cross 2, the Aco2-Aco4-Idh1 3-locus combination (genotype 124) had a MAT of 29 ± 1 d, 8 d later than the 0 class (Table 30). A similar effect on MAT was observed for the Aco2-a homozygotes and the Aco2-a Aco2-a Aco4-b Aco4-b genotype, but not for the Aco2-Dia1 and Aco4-Dia1 2-locus combinations (Tables 28

and 29). Some 3-locus genotypes, however, showed effects that were greater in magnitude and opposite in direction of the effects of the 1- and 2-locus combinations of the 3 loci. For example, the Aco4-b Aco4-b Ap-a Ap-a Pgm1-a Pgm1-a genotype (genotype 256) had a MAT of 40 ± 1 d, about 19 d later than the 0 class, and a HT of 126 ± 5 cm, about 27 cm taller than the 0 class (Table 30). For MAT, Aco4-b homozygotes were 4 d later than the 0 class, Ap-a homozygotes were 8 d earlier, and Pgm1-a homozygotes were 2 d later, so the sum of the 1-locus effects is 2 d earlier. The sum of the effects of the Aco4-Ap (+2 d), Aco4-Pgm1 (+2 d), and Ap-Pgm1 (-7 d) 2-locus combinations was 3 d earlier maturity. None of the effects was as large as the 19 d later MAT observed in the 3-locus combination. For HT, the sum of the 1-locus effects was 18 cm shorter, and for the 2-locus combinations, it was 29 cm shorter, but the 3-locus genotype was 27 cm taller than the 0 class (Tables 28 through 30).

The effects observed for some genotypes in the 4- and 5-locus classes were different from those for any of the 1-locus genotypes alone, but not always different from the effects observed for some of the 2- or 3-locus genotypes that are part of the higher order combinations. For example, in Cross 1, the Aco2-Ap-Pgm1-Pgm2 4-locus combination had a PLT score that was greater than for any of the 1-locus genotypes alone, but it was similar to the effects observed for the Aco2-Pgm1 and Aco2-Pgm2 2-locus combinations (Tables 26, 27, and 28). For Cross 2, the Aco4-Dia1-Ap-Pgm2 4-locus combination had a MAT of 9 ± 1 d, which was different than for any of the 1-locus genotypes, but similar to MAT for the Dia1-Ap-Pgm2 3-locus combination (Tables 28,

30, and 31). There were four different isozyme marker-locus genotypes in the 5-locus class for Cross 2 (Table 32). Two of the genotypes were associated with later MAT, one with earlier MAT, and one had no effect relative to the 0 class. None of the genotypes was associated with decreases in HT or LDG. The Aco4-Idh1-Dia1-Pgm1-MDH 5-locus combination (genotype 23468) had HT and LDG scores similar to the 0-locus class, while the other three genotypes were taller and more prone to lodging. Genotype 23468 was associated with less vining and a more desirable plant type. The other 5-locus genotypes were associated with poorer PLT and greater VNG relative to BC_2F_4-derived lines that had retained no G. soja alleles at any of the isozyme loci that were used as markers. It is difficult to speculate on the kinds of interactions that might occur in the multilocus genotypes.

Some enzyme locus genotypes had phenotypes for MAT and HT that were outside the range of the parents. In Cross 1, some genotypes were later than the G. max parent A80-244036 and some were taller than the G. soja parent PI 326581 (Tables 23 through 27). For Cross 2, there were transgressive segregates in both directions for MAT, and in one direction, shorter than the G. max parent, for HT (Tables 28 through 32). No genotypes had LDG, PLT, or VNG scores that were better than the G. max parent in either cross.

DISCUSSION

The relationships between particular isozyme genotypes and quantitative traits were population specific. This specificity is not surprising because segregation for both marker loci and quantitative trait loci is required to determine possible linkage relationships. The segregation and linkage relationships that will be observed depend upon the number of gene differences and the amount of recombination that can occur between the parental genotypes. Linkage phase also would influence the kinds of associations that were observed. Coupling linkages would be expected to predominate for most traits in interspecific crosses between adapted, agronomically desirable cultivars that have been subjected to many cycles of artificial selection, and wild, weedy, progenitor species.

The opportunity for recombination between the parents is one factor that may be particularly important in interspecific crosses. In soybean, Griffin and Palmer (1987) reported two different estimates of recombination between the Spl and Aco3 loci. The estimate from a G. max x G. soja cross ('A1937' x PI 342622A) was 4.6 ± 0.9%, while the estimate from a G. max x G. max cross (PI 437728 x 'Evans') was 30.6 ± 3.0%. They cited the possibility of cryptic structural heterogeneity between the G. max and G. soja accessions, or the existence of genetic factors affecting the frequency of recombination. In tomato, significant deviations from expected segregation ratios were observed in interspecific crosses (Tanksley et al., 1982), which agreed with other observations in interspecific crosses of tomato (Rick, 1963,

1969) and cotton (Stephens, 1949).

In Cross 1 (A80-244036 x PI 326581), Pgm1 showed a strong association with genes that affected MAT and HT, but only one of the eight BC_2F_1 families in Cross 2 (A81-157007 x PI 342618A) showed such an effect. Palmer et al. (1987) reported the presence of a translocation in PI 342618A. If either the Pgm1 locus or the genes affecting maturity were linked to the interchange break point, it would alter the linkage relationship, which may account for the observed results.

Interactions between loci affecting the quantitative traits were observed in the multilocus enzyme genotypes. Some two-locus genotypes produced effects on the quantitative traits that were not observed in the single-locus analysis, or that were opposite in effect. Similar results were observed in an interspecific backcross in tomato (Tanksley et al., 1982). Tanksley et al. (1982) noted that this relationship suggested that a number of loci affecting quantitative traits were not detected by the single-locus analysis and that the undetected loci were probably highly epistatic, producing both positive and negative results on the character. They concluded that the procedures for detecting quantitative trait loci were biased toward loci with a high degree of additivity.

Because the relationships observed between particular enzyme genotypes and quantitative traits in one population cannot be inferred to exist in all populations, their general application to plant improvement is limited. However, genes that have larger effects on important agronomic characters could be located in different populations using isozymes or other markers. The individual genes affecting

quantitative traits could be introduced into other genetic backgrounds through hybridization or cloning to study gene action and effects in different genetic backgrounds and environments.

When only the numbers of marker loci were considered, lines that were homozygous for G. soja alleles at greater numbers of marker loci were more like the G. soja parent for HT, LDG, PLT, and VNG. Similar trends were observed for both populations. Such relationships would be expected if the marker genes and genes affecting the quantitative traits were distributed throughout the genome. As more marker loci with G. soja alleles are selected, genes linked to the marker region also are included. With a large number of markers, effects of individual marker-locus and multilocus genotypes would be expected to average out and show more general trends. Because the relationships between quantitative traits and numbers of marker loci are not population specific, consideration of numbers of marker loci may be applied generally to plant improvement. For example, marker loci may be useful in an introgression program for recovery of the recurrent parent phenotype while maintaining specific desired alleles from the donor parent. Some theory on the use of marker alleles for the introgression of linked quantitative alleles was discussed by Soller and Plotkin-Hazan (1977), and empirical studies by Tanksley et al. (1981) and Tanksley et al. (1982) showed the utility of isozyme markers in the introgression of exotic germplasm. Identification of marker locus/quantitative trait relationships would allow more efficient utilization of the genetic resources available to plant breeders.

Genes affecting maturity date were associated with specific enzyme

locus genotypes, but MAT showed no relationship with numbers of homozygous marker loci. Some specific enzyme genotypes showed large effects on HT, and smaller effects also were detected for HT, LDG, PLT, and VNG. These observations may be related to the numbers of genes influencing the character and the magnitude of their effects. For example, genes with major effects on maturity and plant height have been identified in soybean (Palmer and Kilen, 1987). If relatively few genes with large effects account for most of the variation observed for a trait, their distribution in the genome will be limited, and an association with numbers of loci would be weak. Maturity belongs in this category. Height, on the other hand, seems to be influenced both by genes with large effects that are detectable in specific associations with marker loci, and by many genes with relatively smaller effects that are distributed throughout the genome. Lodging, plant type, and vining are more general phenotypic characters that are likely influenced by a large number of genes involved in anatomical and physiological processes. These traits showed a relationship primarily with numbers of loci, although some differences among enzyme genotypes were detected.

In this study, six or eight isozyme marker loci were monitored in the two crosses. Linkage data that are available indicate that these loci are independent of one another (Griffin and Palmer, 1987; Palmer and Kilen, 1987). Therefore, it is possible that up to six or eight of the 20 linkage groups in soybean were marked by the isozyme loci. Additional marker loci would increase the applicability and power of marker-based selection schemes. The identification of restriction fragment length polymorphisms as additional markers would allow more

rapid and precise identification of marker locus/quantitative trait relationships and their application to the genetic improvement of soybean.

SUMMARY AND CONCLUSIONS

A study was conducted to examine associations between isozyme marker loci and quantitative traits in soybean. The populations used were two interspecific crosses between the cultivated soybean, Glycine max (L.) Merr., and the wild species, G. soja Sieb. and Zucc. The two species differ widely for many morphological characters and have different alleles at several isozyme loci. The G. max parents were elite lines from the soybean breeding project at Iowa State University, and the G. soja parents were plant introductions from the U.S.S.R. The parents of Cross 1 possessed different alleles at six of the eleven isozyme loci tested: Aco2, Idh2, Ap, Pgm1, Pgm2, and Pgi. The parents of Cross 2 differed for alleles at eight isozyme loci: Aco2, Aco4, Idh1, Dia1, Ap, Pgm1, Pgm2, and MDH. Linkage data that are available indicate that these loci are independent of one another, and potentially six or eight of the 20 linkage groups in soybean were marked.

The objectives of this study were to examine the relationships between agronomic performance and the number of isozyme marker loci that were homozygous for G. soja alleles, and to determine if particular loci or genes linked to them affected specific quantitative traits. Approximately 4,000 BC_2F_4-derived lines obtained by single seed descent from ten BC_2F_1 plants from each cross were evaluated in two replications at two locations for date of maturity (MAT), plant height (HT), lodging (LDG), plant type (PLT), and vining (VNG). Lines were identified that were homozygous for G. soja alleles at different numbers of marker

loci, from zero to five. Within each locus class, there were specific enzyme genotypes, and each enzyme genotype was represented by two to five lines from different BC_2F_1 families.

Individual marker loci were associated with each of the quantitative traits examined. It was shown that the effects of marker locus genotypes on quantitative characters was due to linkage between the marker loci and genes affecting the quantitative traits, rather than due to pleitropic action of the marker genes. The associations with particular marker locus genotypes, however, were population specific. Besides the number of gene differences between the parents of a cross, other factors that may affect the segregation and linkage relationships, particularly in interspecific crosses, are cryptic structural heterogeneity and genetic factors that affect recombination or zygote and seedling survival.

When numbers of marker loci were considered, associations were found with HT, LDG, PLT, and VNG in both populations. Because the relationships are not population specific, consideration of numbers of marker loci may be applied generally to plant improvement. Selection for numbers of recurrent parent alleles in an introgression program would facilitate the recovery of the recurrent parent phenotype, while specific markers could be used to maintain desired alleles from the donor parent.

With relatively few markers representing less than half of the linkage groups in soybean, associations between marker loci and genes affecting quantitative traits were found nonetheless. With these positive results, it is evident that additional markers would increase

the applicability and power of marker-based selection schemes. Development of additional markers like restriction fragment length polymorphisms would make these procedures more powerful and more efficient.

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